

APPENDIX A

BLAST**Basic Local Alignment Search Tool**

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[Edit and Resubmit Save Search Strategies Documented](#)**SEQID40**Results for: **Icl|25193 SEQID40(597aa)**

Your BLAST job specified more than one input sequence. This box lets you choose which input sequence to show BLAST results for.

Icl|25193
Icl|25193**Description**

SEQID40

Molecule type

amino acid

Query Length

597

Database Name

nr

Description

All non-redundant GenBank CDS translations+PDB+SwissProt+PIR+PRF excluding environmental samples from WGS projects

ProgramBLASTP 2.2.24+ [Citation](#)**Reference**

Stephen F. Altschul, Thomas L. Madden, Alejandro A. Schäffer, Jinghui Zhang, Zheng Zhang, Webb Miller, and David J. Lipman (1997), "Gapped BLAST and PSI-BLAST: a new generation of protein database search programs", Nucleic Acids Res. 25:3389-3402.

Reference - compositional score matrix adjustment

Stephen F. Altschul, John C. Wootton, E. Michael Gertz, Richa Agarwala, Aleksandr Morgulis, Alejandro A. Schäffer, and Yi-Kuo Yu (2005) "Protein database searches using compositionally adjusted substitution matrices", FEBS J. 272:5101-5109.

Other reports: [Search Summary](#) [Taxonomy reports](#) [Distance list of results](#) [Multiple alignment](#)[Search Parameters](#)**Search parameter name** **Search parameter value**

Program	blastp
Word size	3
Expect value	10
Hitlist size	100
Gapcosts	11,1
Matrix	BLOSUM62
Filter string	F
Genetic Code	1
Window Size	40
Threshold	11
Composition-based stats	2

Database

Database parameter name **Database parameter value**

Posted date	Sep 26, 2010 5:43 PM
Number of letters	4,071,357,309
Number of sequences	11,921,515
Entrez query	none

Karlin-Altschul statistics

Params **Ungapped** **Gapped**

Lambda	0.318492	0.267
K	0.132452	0.041
H	0.386991	0.14

Results Statistics

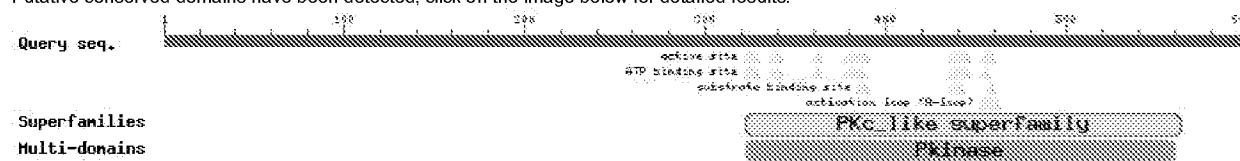
Results Statistics parameter name **Results Statistics parameter value**

Length adjustment	144
Effective length of query	453
Effective length of database	2354659149
Effective search space	1066660594497
Effective search space used	1066660594497

Graphic Summary

Show Conserved Domains

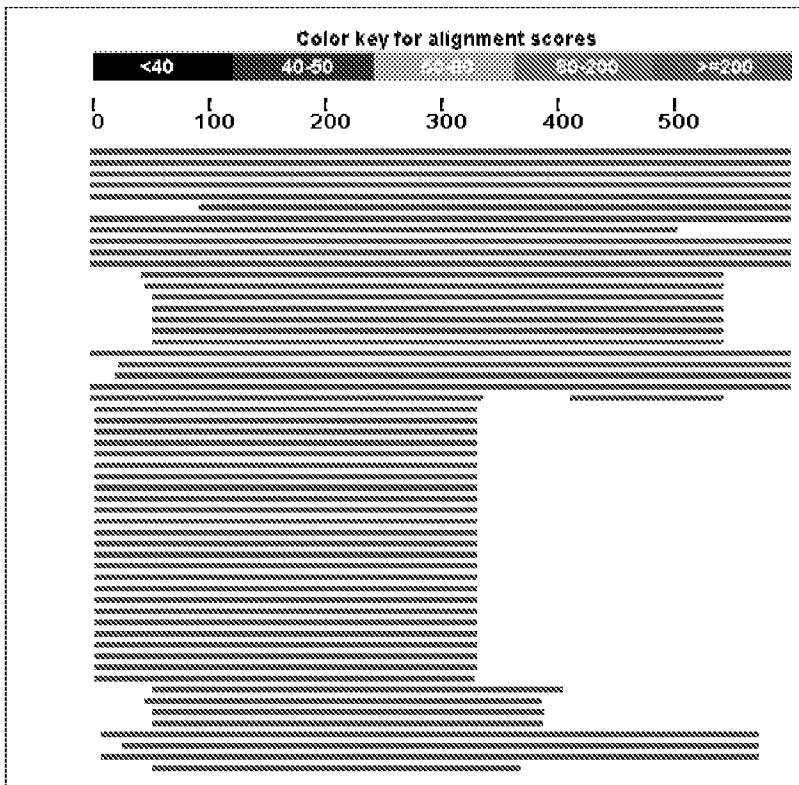
Putative conserved domains have been detected, click on the image below for detailed results.



Distribution of 102 Blast Hits on the Query Sequence

[?]

An overview of the database sequences aligned to the query sequence is shown. The score of each alignment is indicated by one of five different colors, which divides the range of scores into five groups. Multiple alignments on the same database sequence are connected by a striped line. Mousing over a hit sequence causes the definition and score to be shown in the window at the top, clicking on a hit sequence takes the user to the associated alignments. New: This graphic is an overview of database sequences aligned to the query sequence. Alignments are color-coded by score, within one of five score ranges. Multiple alignments on the same database sequence are connected by a dashed line. Mousing over an alignment shows the alignment definition and score in the box at the top. Clicking an alignment displays the alignment detail.



Descriptions

Legend for links to other resources: UniGene GEO Gene Structure Map Viewer PubChem BioAssay
Sequences producing significant alignments:

Accession	Description	Max score	Total score	Query coverage	E value	Links
ABQ888888.1	NFR5a [Glycine max] >gb ADJ19105.1 Nod-factor receptor 5A [Glycine max] >gb ADJ19108.1 Nod-factor receptor 5A [Glycine max]	3058	1058	100%	0.0	
ADJ18188.1	Nod-factor receptor 5A [Glycine max]	3057	1057	100%	0.0	
ADJ18187.1	Nod-factor receptor 5A [Glycine max]	3055	1055	100%	0.0	
ADJ18183.1	Nod-factor receptor 5B [Glycine max]	3029	1029	100%	0.0	
ADJ18181.1	Nod-factor receptor 5B [Glycine max]	3028	1028	100%	0.0	
ABQ888818.1	NFR5b [Glycine max]	869	909	84%	0.0	
CAE02598.1	SYM10 protein [Pisum sativum] >emb CAE02594.1 SYM10 protein [Pisum sativum]	870	870	100%	0.0	
ADQ18118.1	truncated Nod-factor receptor 5A [Glycine max]	868	866	83%	0.0	
CAE02595.1	SYM10 protein [Pisum sativum] >emb CAE02596.1 SYM10 protein [Pisum sativum] >gb ADB45277.1 Nod factor recognition protein [Pisum sativum]	865	865	100%	0.0	
CAE02597.1	Nod-factor receptor 5 [Lotus japonicus] >emb CAE02598.1 Nod-factor receptor 5 [Lotus japonicus]	862	862	100%	0.0	
ABF50224.1	Nod factor perception protein [Medicago truncatula]	839	839	100%	0.0	
CAQ02936.1	LysM-domain containing receptor-like kinase [Medicago truncatula var. truncatula]	749	740	83%	0.0	
CAQ02935.1	LysM-domain containing receptor-like kinase [Medicago truncatula var. truncatula]	733	733	82%	0.0	
CAQ02933.1	LysM-domain containing receptor-like kinase [Medicago truncatula var. truncatula] >emb CAO02934.1 LysM-domain containing receptor-like kinase [Medicago truncatula var. truncatula] >emb CAO02935.1 LysM-domain containing receptor-like kinase [Medicago truncatula var. truncatula] >emb CAO02938.1 LysM-domain containing receptor-like kinase [Medicago truncatula var. truncatula] >emb CAO02939.1 LysM-domain containing receptor-like kinase [Medicago truncatula var. truncatula] >emb CAO02952.1 LysM-domain containing receptor-like kinase [Medicago truncatula var. truncatula] >emb CAO02953.1 LysM-domain containing receptor-like kinase [Medicago truncatula var. truncatula] >emb CAO02955.1 LysM-domain containing receptor-like kinase [Medicago truncatula var. truncatula] >emb CAO02957.1 LysM-domain containing receptor-like kinase [Medicago truncatula var. truncatula] >emb CAO02959.1 LysM-domain containing receptor-like kinase [Medicago truncatula var. truncatula] >emb CAO02967.1 LysM-domain containing receptor-like kinase [Medicago truncatula var. truncatula] >emb CAO02971.1 LysM-domain containing receptor-like kinase [Medicago truncatula var. truncatula] >emb CAO02972.1 LysM-domain containing receptor-like kinase [Medicago truncatula var. truncatula] >emb CAO02973.1 LysM-domain containing receptor-like kinase [Medicago truncatula var. truncatula]	725	725	81%	0.0	
CAQ02940.1	LysM-domain containing receptor-like kinase [Medicago truncatula var. truncatula]	723	723	81%	0.0	
CAQ02951.1	LysM-domain containing receptor-like kinase [Medicago truncatula var. truncatula]	723	723	81%	0.0	
CAQ02951.1	LysM-domain containing receptor-like kinase [Medicago truncatula var. truncatula] >emb CAO02970.1 LysM-domain containing receptor-like kinase [Medicago truncatula var. truncatula]	722	722	81%	0.0	
CAQ02955.1	LysM-domain containing receptor-like kinase [Medicago tornata]	718	718	81%	0.0	
BAI79275.1	LysM type receptor kinase [Lotus japonicus] >dbj BAI79285.1 LysM type receptor kinase [Lotus japonicus]	708	706	100%	0.0	
XP_002259472.1	PREDICTED: hypothetical protein [Vitis vinifera] >emb CBI17584.3 unnamed protein product [Vitis vinifera]	643	643	95%	0.0	
XP_002259477.1	serine-threonine protein kinase, plant-type, putative [Ricinus communis] >gb EEF29112.1 serine-threonine protein kinase, plant-type, putative [Ricinus communis]	618	618	96%	6e-175	
XP_002333299.1	predicted protein [Populus trichocarpa] >gb EEE90648.1 predicted protein [Populus trichocarpa]	595	595	100%	7e-168	
ADJ18189.1	truncated Nod-factor receptor 5A [Glycine max]	536	536	56%	4e-150	
BAG885147.1	Nod factor receptor protein [Glycine soja]	519	519	54%	4e-145	
BAG885148.1	Nod factor receptor protein [Glycine soja] >dbj BAG85149.1 Nod factor receptor protein [Glycine soja] >dbj BAG85156.1 Nod factor receptor protein [Glycine soja] >dbj BAG85159.1 Nod factor receptor protein [Glycine max] >dbj BAG85160.1 Nod factor receptor protein [Glycine max] >dbj BAG85161.1 Nod factor receptor protein [Glycine max] >dbj BAG85162.1 Nod factor receptor protein [Glycine max] >dbj BAG85165.1 Nod factor receptor protein [Glycine max] >dbj BAG85168.1 Nod factor receptor protein [Glycine max] >dbj BAG85171.1 Nod factor receptor protein [Glycine max] >dbj BAG85174.1 Nod factor receptor protein [Glycine max] >dbj BAG85177.1 Nod factor receptor protein [Glycine max] >dbj BAG85179.1 Nod factor receptor protein [Glycine max] >dbj BAG85180.1 Nod factor receptor protein [Glycine max]	516	516	54%	3e-144	
BAG885152.1	Nod factor receptor protein [Glycine soja]	516	516	54%	5e-144	
BAG885158.1	Nod factor receptor protein [Glycine soja]	515	515	54%	5e-144	
BAG885178.1	Nod factor receptor protein [Glycine max]	514	514	54%	9e-144	
BAG885144.1	Nod factor receptor protein [Glycine soja] >dbj BAG85145.1 Nod factor receptor protein [Glycine soja]	514	514	54%	1e-143	
BAG885179.1	Nod factor receptor protein [Glycine max]	514	514	54%	1e-143	
BAG885187.1	Nod factor receptor protein [Glycine max]	514	514	54%	1e-143	
BAG885186.1	Nod factor receptor protein [Glycine max]	514	514	54%	1e-143	
BAG885183.1	Nod factor receptor protein [Glycine soja]	514	514	54%	1e-143	
BAG885186.1	Nod factor receptor protein [Glycine soja]	514	514	54%	1e-143	

BAG885182.1	Nod factor receptor protein [Glycine soja]	514	514	54%	2e-143	
BAG885188.1	Nod factor receptor protein [Glycine max]	514	514	54%	2e-143	6
BAG885172.1	Nod factor receptor protein [Glycine max]	514	514	54%	2e-143	
BAG885182.1	Nod factor receptor protein [Glycine soja]	513	513	54%	2e-143	
BAG885175.1	Nod factor receptor protein [Glycine max]	513	513	54%	3e-143	
BAG885180.1	Nod factor receptor protein [Glycine soja]	513	513	54%	3e-143	
BAG885173.1	Nod factor receptor protein [Glycine max]	513	513	54%	3e-143	
BAG885187.1	Nod factor receptor protein [Glycine soja]	513	513	54%	4e-143	
BAG885176.1	Nod factor receptor protein [Glycine max]	511	511	54%	8e-143	
BAG885188.1	Nod factor receptor protein [Glycine soja]	511	511	54%	1e-142	
BAG885183.1	Nod factor receptor protein [Glycine max]	511	511	54%	2e-142	
BAG885186.1	Nod factor receptor protein [Glycine soja]	509	509	54%	4e-142	
BAG885169.1	Nod factor receptor protein [Glycine max]	507	507	54%	2e-141	
BAG885186.1	Nod factor receptor protein [Glycine max]	501	501	54%	9e-140	
CAD028388.1	LysM-domain containing receptor-like kinase [Medicago truncatula var. truncatula]	482	482	58%	8e-134	
CAD028388.1	LysM-domain containing receptor-like kinase [Medicago truncatula var. truncatula]	465	465	56%	7e-129	
CAD028382.1	LysM-domain containing receptor-like kinase [Medicago truncatula var. truncatula]	462	462	56%	4e-128	
CAD028389.1	LysM-domain containing receptor-like kinase [Medicago truncatula var. truncatula]	458	458	55%	9e-127	
AAN19130.1	Putative protein kinase [Oryza sativa Japonica Group] >gb ABF94815.1 Protein kinase domain containing protein [Oryza sativa (japonica cultivar-group)] >gb EAZ26175.1 hypothetical protein OsJ_10042 [Oryza sativa Japonica Group]	426	426	93%	5e-117	
XP_892488226.1	hypothetical protein SORBIDRAFT_01g042230 [Sorghum bicolor] >gb EER95234.1 hypothetical protein SORBIDRAFT_01g042230 [Sorghum bicolor]	426	426	90%	5e-117	6
SAV89188.1	hypothetical protein OsI_10648 [Oryza sativa Indica Group]	424	424	93%	2e-116	
CAQ82253.1	LysM-domain containing receptor-like kinase [Medicago truncatula var. truncatula]	417	417	52%	3e-114	
CAQ82264.1	LysM-domain containing receptor-like kinase [Medicago truncatula var. truncatula] >emb CAO02968.1 LysM-domain containing receptor-like kinase [Medicago truncatula var. truncatula]	414	414	52%	1e-113	
CAQ82264.1	LysM-domain containing receptor-like kinase [Medicago truncatula var. truncatula]	408	408	51%	1e-111	
CAQ82264.1	LysM-domain containing receptor-like kinase [Medicago truncatula var. truncatula]	404	404	51%	2e-110	
CAD028362.1	LysM-domain containing receptor-like kinase [Medicago truncatula var. truncatula]	400	400	51%	3e-109	
XP_892817928.1	serine-threonine protein kinase, plant-type, putative [Ricinus communis] >gb EEF45192.1 serine-threonine protein kinase, plant-type, putative [Ricinus communis]	356	356	89%	6e-96	6
XP_892280079.1	PREDICTED: hypothetical protein [Vitis vinifera]	348	348	89%	1e-93	6
CB129359.3	unnamed protein product [Vitis vinifera]	343	343	89%	3e-92	
AAV89791.1	SYM10-like protein [Galega orientalis]	336	336	40%	4e-90	
ABX170633.3	unknown [Picea sitchensis]	333	333	77%	3e-89	
CAN66782.1	hypothetical protein [Vitis vinifera]	328	328	89%	1e-87	
XP_891757824.1	predicted protein [Physcomitrella patens subsp. patens] >gb EDQ67338.1 predicted protein [Physcomitrella patens subsp. patens]	309	309	91%	8e-82	6
XP_892311853.1	predicted protein [Populus trichocarpa] >gb EEE89020.1 predicted protein [Populus trichocarpa]	308	308	76%	2e-81	6
SAV87982.1	hypothetical protein OsI_08480 [Oryza sativa Indica Group]	299	299	88%	8e-79	
CAQ022959.1	LysM-domain containing receptor-like kinase [Medicago truncatula var. truncatula]	298	298	40%	2e-78	
BAI79276.1	LysM type receptor kinase [Lotus japonicus]	293	293	92%	5e-77	
XP_891753889.1	predicted protein [Physcomitrella patens subsp. patens] >gb EDQ51621.1 predicted protein [Physcomitrella patens subsp. patens]	285	285	90%	1e-74	6
XP_892328891.1	predicted protein [Populus trichocarpa] >gb EEE73651.1 predicted protein [Populus trichocarpa]	285	285	86%	1e-74	6
XP_892817926.1	kinase, putative [Ricinus communis] >gb EEF52943.1 kinase, putative [Ricinus communis]	284	284	86%	2e-74	6
SAV82277.1	LysM type receptor kinase [Lotus japonicus] >dbj BAI79287.1 LysM type receptor kinase [Lotus japonicus]	283	283	96%	5e-74	
CB117583.3	unnamed protein product [Vitis vinifera]	542	542	93%	3e-72	
XP_882880885.1	hypothetical protein SELMODRAFT_11326 [Selaginella moellendorffii] >gb EFJ08078.1 hypothetical protein SELMODRAFT_11326 [Selaginella moellendorffii]	275	275	89%	2e-71	6
XP_892975494.1	hypothetical protein SELMODRAFT_11327 [Selaginella moellendorffii] >gb EFJ24716.1 hypothetical protein SELMODRAFT_11327 [Selaginella moellendorffii]	273	273	89%	4e-71	6
XP_892277321.1	PREDICTED: hypothetical protein [Vitis vinifera]	272	272	89%	8e-71	6
XP_892328442.1	PREDICTED: hypothetical protein [Vitis vinifera]	268	268	93%	2e-69	6
BAI79276.1	LysM type receptor kinase [Lotus japonicus]	268	268	97%	2e-69	
BAI79285.1	LysM type receptor kinase [Lotus japonicus]	267	267	97%	3e-69	
XP_892553223.1	serine-threonine protein kinase, plant-type, putative [Ricinus communis] >gb EEF29111.1 serine-threonine protein kinase, plant-type, putative [Ricinus communis]	264	264	88%	3e-68	6
XP_892553228.1	BRASSINOSTEROID INSENSITIVE 1-associated receptor kinase 1 precursor, putative [Ricinus communis] >gb EEF29110.1 BRASSINOSTEROID INSENSITIVE 1-associated receptor kinase 1 precursor, putative [Ricinus communis]	263	263	91%	4e-68	6
XP_892553226.1	BRASSINOSTEROID INSENSITIVE 1-associated receptor kinase 1 precursor, putative [Ricinus communis] >gb EEF39869.1 BRASSINOSTEROID INSENSITIVE 1-associated receptor kinase 1 precursor, putative [Ricinus communis]	262	262	90%	1e-67	6
CB146796.3	unnamed protein product [Vitis vinifera]	336	336	85%	9e-67	

XP_0022518333.1	serine-threonine protein kinase, plant-type, putative [Ricinus communis] >gb EEF52520.1	258	258	86%	2e-66	
XP_0022518333.1	PREDICTED: hypothetical protein [Vitis vinifera]	256	256	86%	9e-66	
XP_0022518333.1	PREDICTED: hypothetical protein [Vitis vinifera]	254	254	90%	2e-65	
XP_0022518333.1	predicted protein [Populus trichocarpa] >gb EEE91227.1 predicted protein [Populus trichocarpa]	253	253	86%	6e-65	
ABQ59812.1	LYK4 [Glycine max]	253	253	95%	8e-65	
XP_0022518333.1	predicted protein [Populus trichocarpa] >gb EEE75190.1 predicted protein [Populus trichocarpa]	249	249	86%	9e-64	
Os06g0625200 [Oryza sativa Japonica Group] >dbj BAD35689.1 receptor protein kinase-like [Oryza sativa Japonica Group] >dbj BAD37734.1 receptor protein kinase-like [Oryza sativa Japonica Group] >dbj BAF20024.1 Os06g0625200 [Oryza sativa Japonica Group] >gb EAZ37689.1 hypothetical protein OsJ_22029 [Oryza sativa Japonica Group]	242	242	86%	8e-62		
XP_0022518333.1	predicted protein [Populus trichocarpa] >gb EEE94826.1 predicted protein [Populus trichocarpa]	239	239	86%	7e-61	
CAQ028661.1	LysM-domain containing receptor-like kinase [Medicago truncatula var. truncatula]	238	238	21%	2e-60	
XP_0022518333.1	ATP binding protein, putative [Ricinus communis] >gb EEF50927.1 ATP binding protein, putative [Ricinus communis]	236	236	91%	7e-60	
NP_00666882.2	CERK1 (CHITIN ELICITOR RECEPTOR KINASE 1); kinase/receptor signaling protein/transmembrane receptor protein kinase [Arabidopsis thaliana] >dbj BAF92788.1 chitin elicitor receptor kinase 1 [Arabidopsis thaliana]	229	229	81%	1e-57	
XP_0022518333.1	predicted protein [Populus trichocarpa] >gb EEE84903.1 predicted protein [Populus trichocarpa]	224	224	91%	2e-56	
XP_0022518333.1	PREDICTED: hypothetical protein [Vitis vinifera]	224	224	97%	3e-56	
CBM60556.3	unnamed protein product [Vitis vinifera]	224	224	97%	4e-56	

Alignments

Select All Get selected sequences Distance tree of results Multiple alignment

>gb ABQ59609.1 NFR5a [Glycine max]						
gb ADJ19105.1  Nod-factor receptor 5A [Glycine max]						
gb ADJ19108.1  Nod-factor receptor 5A [Glycine max]						
Length=598						
Score = 1058 bits (2737), Expect = 0.0, Method: Compositional matrix adjust.						
Identities = 527/598 (88%), Positives = 560/598 (93%), Gaps = 1/598 (0%)						
Query 1 MAVFFVSLTGLAQIYLVYVLMFF-TCIEAQSQQTNGTNFSCPSNSPPSCETYVTYISQSPN 59						
Sbjct 1 MAVFF L L +QIL +V+M F T I AQSQQ N TNFSCPS+SPPSCETYVTYI+QSPN 60						
Query 60 FLSLTSVSNIFDTSPLSIIARASNLQHEEDKLI+PGQVLLIPVTCGCTGNRSFANISYEINQ 119						
Sbjct 61 FLSLTSVSNIFDTSPLSIIARASNL+ +DKLT+ QVLL+PVTCCGTGNRSFANISYEINQ 120						
Query 120 GDSFYFVATTLYQNLTNWHAVMIDLNPGLSQFTLPIGLIQVVIPLFCKCPSKNQLDRGIKYL 179						
Sbjct 121 GDSFYFVATTLYQNLTNWHAVMIDLNPGLSQFTLPIGLIQVVIPLFCKCPSKNQLDRGIKYL 180						
Query 180 ITHWQPNNDNVSVFVSNKLGASPQDLSENNYQGQNTAAASNLPVLPVTLPPDIQSPSDG 239						
Sbjct 181 ITYYWKPGDNVSVLSDKFGASPEDIMSENNYQGQNTAAASNLPVLPVTLPPDIQSPSDG 240						
Query 240 RKHRIGLPVIIGISLGCTLLVVSAIILVCVCLKMKSLNRSASSAETADKLISGVSGYV 299						
Sbjct 241 RKHRIGLPVIIGISLGCTLLVV+ A+LLV V CLKMK+LNRSASSAETADKLISGVSGYV 300						
Query 300 SKPTMYETGAIATEAMNLSEQCKIGESVYKANIEGKVLAVKRFKEDDVTEELKILQKVNHG 359						
Sbjct 301 SKPTMYETAI+EATMNLSEQCKIGESVYKANIEGKVLAVKRFKEDDVTEELKILQKVNHG 360						
Query 360 NLVKLMGVSSENDDNCNCFVYYEYAENGSLLEEWLFAKSCSETNSNRTSLTWQRISIAVDVS 419						
Sbjct 361 NLVKLMGVSSENDDNCNCFVYYEYAENGSL+EWLP+KSCS+TSNS_ SLTWCQRIS+AVDV+ 420						
Query 420 MGLQYMHEHAYPRIVHRDITSSNILLDSNFKAARIANFSMARTFTNPMMSKIDVFAFGVVL 479						
Sbjct 421 MGLQYMHEHAYPRIVHRDITSSNILLDSNFKAARIANFSMARTFTNPMMKIDVFAFGVVL 480						
Query 480 IELLTGRKAMTTKENGEVVMLWKDIWKFIDQEENREERLKRWMDPKL++YPIDYALSLA 539						
Sbjct 481 IELLTGRKAMTTKENGEVVMLWKDIWKFIDQEENREERLKRWMDPKLESYYYIDYALSLA 540						
Query 540 SLAVNCTADKSLSRPTIAEIVLSSLTQPSPATLERSLTSSGLDVEATQIVTSIAR 597						
Sbjct 541 SLAVNCTADKSLSRPTIAEIVLSSLTQPSPATLERSLTSSGLDVEATQIVTSIAR 598						

>gb|ADJ19106.1|  Nod-factor receptor 5A [Glycine max]

Length=598

GENE ID: 100498858 NFR5a | Nod-factor receptor 5A [Glycine max]
(10 or fewer PubMed links)

Score = 1057 bits (2733), Expect = 0.0, Method: Compositional matrix adjust.						
Identities = 526/598 (87%), Positives = 560/598 (93%), Gaps = 1/598 (0%)						
Query 1 MAVFFVSLTGLAQIYLVYVLMFF-TCIEAQSQQTNGTNFSCPSNSPPSCETYVTYISQSPN 59						
Sbjct 1 MAVFF L L +QIL +V+M F T I AQSQQ N TNFSCPS+SPPSCETYVTYI+QSPN 60						

Query	60	FSLTSVSNIFDTSPLSIARASN LQHEEDKLIPGQVLLIPVTCGCTGNRSFANISYEINQ	119
Sbjct	61	FLSLTNISNIFDTSPLSIARASNLEPMDDKLVKDQVLLPVTGCTGNRSFANISYEINQ	120
Query	120	GDSFYFVATTLYQNLTNWHAVMMDLNPGLSQFTLPIGIQVVIPLFCKCPSKNQLDRGIKYL	179
Sbjct	121	GDSFYFVATTSYENLTNWRAVMDLNVPVSPNKLPIGIQVVFPLFCKCPSKNQLDKEIKYL	180
Query	180	ITHWQPNDNVSFVSNKLGASPQDILSENNYQGNFTAASNLPVLIPVTLPLDIQSPSDG	239
Sbjct	181	ITYWVKPGDNVSIVSDKFAGSPEDIMSENNYQGNFTAANNLPVLIPVTRLPVLAARSPSDG	240
Query	240	RKHIGLPIIIGISLGCTLLVVSAILLVCVCLKMKS LNRSSAETADKL LSGVGSGYV	299
Sbjct	241	RKGGLPVIIGISLGCTLLVLVLA VLLVVYVCLKMKT LNRSSAETADKL LSGVGSGYV	300
Query	300	SKPTMYETGAI EATMNL SEQCKI GESVYKANIEGKVLA VKRKFEDVTEELK ILQKVNHG	359
Sbjct	301	SKPTMYET AI+EATMNL SEQCKI GESVYKANIEGKVLA VKRKFEDVTEELK ILQKVNHG	360
Query	360	NLVKLMGVSSNDNGNCV VVYE AENGSL EEWLF AKSCSETNSRTS LTWCQRISIAVDVS	419
Sbjct	361	NLVKLMGVSSNDNGNCV VVYE AENGSL+EWL+F+KSCS+TSNSR SLTW CQRIS+AVDV+	420
Query	420	MGLQYMHEHAYPRIVHRDITSSNILLDSNFKA KIANFSMARTFTNPMM SKIDVFAFGVVL	479
Sbjct	421	MGLQYMHEHAYPRIVHRDITSSNILLDSNFKA KIANFSMARTFTNPMM SKIDVFAFGVVL	480
Query	480	I ELLTGRKAMTTKENGEVVMLW KDIW KIFDQEENREERL R KWDMPKLDNYY PIDYALSLA	539
Sbjct	481	I ELLTGRKAVTTKENGEVVMLW KDIW KIFDQEENREERL R KWDMPKLESYY PIDYALSLA	540
Query	540	SLAVNCTADKSLSRPTIAEIVLSSLT QPSPATLERSLTSSGLDVEATQIVTSIAR	597
Sbjct	541	SLAVNCTADKSLSRPTIAEIVLSSLT QPSPATLERSLTSSGLDVEATQIVTSIAR	598

>gb|ADJ19107.1| Nod-factor receptor 5A [Glycine max]
Length=598

GENE ID: 100498858 NFR5a | Nod-factor receptor 5A [Glycine max]
(10 or fewer PubMed links)

Score = 1055 bits (2728), Expect = 0.0, Method: Compositional matrix adjust.
Identities = 525/598 (87%), Positives = 560/598 (93%), Gaps = 1/598 (0%)

Query	1	MAVFFVSLTGAQI LYV VLMFF-TCIEAQSQQTNGTNFSCPNSPPSCETYV TYI SQSPN	59
Sbjct	1	MAVFFPFLPLHSQ ILCVIMLFSTNIVAQSQQDNRTNFSCP SDPS PSCETYV TYI AQSPN	60
Query	60	FSLTSVSNIFDTSPLSIARASN LQHEEDKLIPGQVLLIPVTCGCTGNRSFANISYEINQ	119
Sbjct	61	FSLTNISNIFDTSPLSIARASNLEPMDDKLVKDQVLLPVTGCTGNRSFANISYEINQ	120
Query	120	GDSFYFVATTLYQNLTNWHAVMMDLNPGLSQFTLPIGIQVVIPLFCKCPSKNQLDRGIKYL	179
Sbjct	121	GDSFYFVATTSYENLTNWRAVMDLNVPVSPNKLPIGIQVVFPLFCKCPSKNQLDKEIKYL	180
Query	180	ITHWQPNDNVSFVSNKLGASPQDILSENNYQGNFTAASNLPVLIPVTLPLDIQSPSDG	239
Sbjct	181	ITYWVKPGDNVSIVSDKFAGSPEDIMSENNYQGNFTAANNLPVLIPVTRLPVLAARSPSDG	240
Query	240	RKHIGLPIIIGISLGCTLLVVSAILLVCVCLKMKS LNRSSAETADKL LSGVGSGYV	299
Sbjct	241	RKGGLPVIIGISLGCTLLVLVLA VLLVVYVCLKMKT LNRSSAETADKL LSGVGSGYV	300
Query	300	SKPTMYETGAI EATMNL SEQCKI GESVYKANIEGKVLA VKRKFEDVTEELK ILQKVNHG	359
Sbjct	301	SKPTMYET AI+EATMNL SEQCKI GESVYKANIEGKVLA VKRKFEDVTEELK ILQKVNHG	360
Query	360	NLVKLMGVSSNDNGNCV VVYE AENGSL EEWLF AKSCSETNSRTS LTWCQRISIAVDVS	419
Sbjct	361	NLVKLMGVSSNDNGNCV VVYE AENGSL+EWL+F+KSCS+TSNSR SLTW CQRIS+AVDV+	420
Query	420	MGLQYMHEHAYPRIVHRDITSSNILLDSNFKA KIANFSMARTFTNPMM SKIDVFAFGVVL	479
Sbjct	421	MGLQYMHEHAYPRIVHRDITSSNILLDSNFKA KIANFSMARTFTNPMM SKIDVFAFGVVL	480
Query	480	I ELLTGRKAMTTKENGEVVMLW KDIW KIFDQEENREERL R KWDMPKLDNYY PIDYALSLA	539
Sbjct	481	I ELLTGRKAVTTKENGEVVMLW KDIW KIFDQEENREERL R KWDMPKLESYY PIDYALSLA	540
Query	540	SLAVNCTADKSLSRPTIAEIVLSSLT QPSPATLERSLTSSGLDVEATQIVTSIAR	597
Sbjct	541	SLAVNCTADKSLSRPTIAEIVLSSLT QPSPATLERSLTSSGLDVEATQIVTSIAR	598

>gb|ADJ19112.1| Nod-factor receptor 5B [Glycine max]
Length=599

GENE ID: 100498857 NFR5b | Nod-factor receptor 5B [Glycine max]
(10 or fewer PubMed links)

Score = 1029 bits (2661), Expect = 0.0, Method: Compositional matrix adjust.
Identities = 530/599 (88%), Positives = 556/599 (92%), Gaps = 2/599 (0%)

Query	1	MAVFFVSLTGAQI LYV VLM-FFTCIEAQSQQTNGTNFSCPNSPPSC-ETV VTYI SQSP	58
Sbjct	1	MAVFFSFLPLRSQ ILCVIMLFSTNIVAQSQQTNETNFSCP SDPS PSCETV VTYI AQSP	60
Query	59	NFLSLTSVSNIFDTSPLSIARASN LQHEEDKLIPGQVLLIPVTCGCTGNRSFANISYEIN	118
Sbjct	61	NFLSLTSVSNIFDTSPLSIARASN E+DKLI QVLLIPVTCGCTGNRSFANISYEIN	120
Query	119	QGDSFYFVATTLYQNLTNWHAVMMDLNPGQLSQFTLPIGIQVVIPLFCKCPSKNQLDRGIKY	178
		GDSFYFVATT Y+NLTNW VMDLNP LS TLPIGI QVVFPLFCKCPSKNQLD+GIKY	

Objct	121	PGDSFYFVATTSYENLTNWRVVMDLNPSLSPNTLPIGIQVVFPLFKCPSKNQLDKGIKY	180
Query	179	LITHVWQPNDNSVFSVSNKLGASPQDILSENNYQGNFTAASNLPVLPVTLLPDLIQSPSD	238
Objct	181	LITVWQPNDNSLVSEKEGASEPDILSENNYQGNFTAANNLPVLIPVTRLPVLAQSPSD	240
Query	239	GRKHRIGLPVIIGISLGCTLLVVVSAILLVCVCLMKMSLNRSASSAETADKLLSGVSGY	298
		RK I LPVIIGISLGCTLLVVV A+LLV V CLK+KSLNRSSASSAETADKLLSGVSGY	
Objct	241	VRKGIRLPLVIIIGISLGCTLLVVVLAVLILVYVYCLIKIKSLNRSSASSAETADKLLSGVSGY	300
Query	299	VSKPTMYETGAILEATMNLSEQCKIGESVYKANIEGKVLAVKRFKEDVTEELKILQKVNH	358
Objct	301	VSKPTMYETDAIMEATMNLSEQCKIGESVYKANIEGKVLAVKRFKENVTEELKILQKVNH	360
Query	359	GNLVKLMGVSSDNDGNCFVVYEEAENGSLLEEWFAKSCSETNSRSTS LTWCQRISIAVDV	418
Objct	361	GNLVKLMGVSSDNDGNCFVVYEEAENGSLLEEWFAKSCSETNSRSTS LTWCQRISIAVDV	420
Query	419	SMGLQYMHEHAYPRIVHRDITSSNILLDSNFKAKIANFSMARTFTNPMMMSKIDVFAFGVV	478
		+MGLQYMHEHAYPRIVHRDI SSNILLDSNFKAKIANFSMARTFTNP M KIDVFAFGVV	
Objct	421	AMGLQYMHEHAYPRIVHRDIASSNILLDSNFKAKIANFSMARTFTNPPTMPKIDVFAFGVV	480
Query	479	LIELLTGRKAMTTKENGEVVMLWKDIWKFIDQEENREERLKWMDPKLDNYYPIDYALSL	538
		LIELLTGRKAMTTKENGEVVMLWKDIWKFIDQEENREERLKWMDPKLDNYYPIDYALSL	
Objct	481	LIELLTGRKAMTTKENGEVVMLWKDIWKFIDQEENREERLKWMDPKLESYYPIDYALSL	540
Query	539	ASLAVNCTADKSLSRPTIAEIVLSSLTQPSPATLERSLTSSGLDVEATQIVTSISAR	597
		ASLAVNCTADKSLSR TIAEIVLSSLTQPSPATLERSLTSSGLDVEATQIVTSI+AR	
Objct	541	ASLAVNCTADKSLSRSTIAEIVLSSLTQPSPATLERSLTSSGLDVEATQIVTSIAAR	599

>gb|ADJ19111.1| Nod-factor receptor 5B [Glycine max]
Length=599

Gene ID: 100498857 NFR5b | Nod-factor receptor 5B [Glycine max]
(10 or fewer PubMed links)

Score = 1028 bits (2657), Expect = 0.0, Method: Compositional matrix adjust.	
Identities = 529/599 (88%), Positives = 555/599 (92%), Gaps = 2/599 (0%)	
Query 1 MAVFFFVSLTLGAQILYVVL - FFTCIEAQSQQTNGTNFSCPSNSPPSC-ETYVTVYISQSP 58	
Objct 1 MAVFF L L +QIL +VLM FFT I AQSQQTN TNFSCPS+SPP ETYVTVYI+QSP 60	
Query 59 NFLSLTSVSNIFDTSPLSIARASNQHQEEDEKLIPGQVLLIPVTCGCTGNRSFANISYEIN 118	
Objct 61 NFLSLTS-SNIFDTSPLSIARASN+ E+DKLI QVLLIPVTCGCTGNRSFANISYEIN 120	
Query 119 QGDIFYFVATTLYQNLTNWHAVMDDLNPGLSQFTLPIGIQVVIPLFCKCP SKNQLDRGIKY 178	
Objct 121 PGDIFYFVATT Y+NLTNW VMDLNP LS TLPIGIQVW PLFCKCP SKNQL+GIKY 180	
Query 179 LITHVWQPNDNSVFSVSNKLGASPQDILSENNYQGNFTAASNLPVLPVTLLPDLIQSPSD 238	
Objct 181 LITVWQPNDNSLVSEKGASPEDILSENNYQGNFTAANNLPVLIPVTRLPVLAQSPSD 240	
Query 239 GRKHRIGLPVIIGISLGCTLLVVVSAILLVCVCLMKMSLNRSASSAETADKLLSGVSGY	
	RK I LPVIIGISLGCTLLVVV A+LLV V CLK+KSLNRSSASSAETADKLLSGVSGY
Objct 241 VRKGIRLPLVIIIGISLGCTLLVVVLAVLILVYVYCLIKIKSLNRSSASSAETADKLLSGVSGY 300	
Query 299 VSKPTMYETGAILEATMNLSEQCKIGESVYKANIEGKVLAVKRFKEDVTEELKILQKVNH	
	VSKPTMYET AI+EATMNLSEQCKIGESVYKANIEGKVLAVKRFKE+VTEELKILQKVNH
Objct 301 VSKPTMYETDAIMEATMNLSEQCKIGESVYKANIEGKVLAVKRFKENVTEELKILQKVNH 360	
Query 359 GN LVKLMGVSSDNDGNCFVVYEEAENGSLLEEWFAKSCSETNSRSTS LTWCQRISIAVDV	
	GN LVKLMGVSSDNDGNCFVVYEEAENGSLLEEWFAKSCSETNSRSTS LTWCQRISIAVDV
Objct 361 GN LVKLMGVSSDNDGNCFVVYEEAENGSLLEEWFAKSCSETNSRSTS LTWCQRISIAVDV 420	
Query 419 SMGLQYMHEHAYPRIVHRDITSSNILLDSNFKAKIANFSMARTFTNPMMMSKIDVFAFGVV	
	+MGLQYMHEHAYPRIVHRDI SSNILLDSNFKAKIANFSMARTFTNP M KIDVFAFGVV
Objct 421 AMGLQYMHEHAYPRIVHRDIASSNILLDSNFKAKIANFSMARTFTNPPTMPKIDVFAFGVV 480	
Query 479 LIELLTGRKAMTTKENGEVVMLWKDIWKFIDQEENREERLKWMDPKLDNYYPIDYALSL	
	LIELLTGRKAMTTKENGEVVMLWKDIWKFIDQEENREERLKWMDPKLDNYYPIDYALSL
Objct 481 LIELLTGRKAMTTKENGEVVMLWKDIWKFIDQEENREERLKWMDPKLESYYPIDYALSL 540	
Query 539 ASLAVNCTADKSLSRPTIAEIVLSSLTQPSPATLERSLTSSGLDVEATQIVTSISAR	
	ASLAVNCTADKSLSR TIAEIVLSSLTQPSP TLERSLTSSGLDVEATQIVTSI+AR
Objct 541 ASLAVNCTADKSLSRSTIAEIVLSSLTQPSPATLERSLTSSGLDVEATQIVTSIAAR 599	

>gb|ABQ59613.1| NFR5b [Glycine max]
Length=515

Score = 909 bits (2348), Expect = 0.0, Method: Compositional matrix adjust.
Identities = 454/504 (90%), Positives = 474/504 (94%), Gaps = 0/504 (0%)

Query 94 QVLLIPVTCGCTGNRSFANISYEINQGDIFYFVATTLYQNLTNWHAVMDDLNPGLSQFTLP 153
Objct 12 QVLLIPVTCGCTGNRSFANISYEIN GDSF FVATT Y+NLTNW VMDLNP LS TLP 71
Query 154 IGIQVVIPLFCKCP SKNQLDRGIKYLITHWQPNNDNSVFSVSNKLGASPQDILSENNYQGN 213
Objct 72 IGIQVW PLFCKCP SKNQLD+GIKYLIT+WVQP+DNVS VS K GASPDILSENNYQGN 131
Query 214 FTAASNLPVLPVTLLPDLIQSPSDGRKHRIGLPVIIGISLGCTLLVVVSAILLVCVCL 273
Objct 132 FTAANNLPVLPVTLPVLAQFPSDVRKGGIRLPLVIIIGISLGCTLLVVVLAVLILVYVYCL 191
Query 274 KMKS LNRSSASSAETADKLLSGVSGYVSKPTMYETGAILEATMNLSEQCKIGESVYKANIE 333
Objct 192 KIKS LNRSSASSAETADKLLSGVSGYVSKPTMYET AI+EATMNLSEQCKIGESVYKANIE 251
Query 334 GKVLAVKRFKEDTEELKILQVNHNGLVKLMGVSSDNDGNCFVVYEEAENGSLLEWLFA 393
Objct 252 GKVLAVKRFKE+VTEELKILQVNHNGLVKLMGVSSDNDGNCFVVYEEAENGSLDEWLFA 311

Query	394	KCSETNSRTSLTWCQRISIAVDVSMGLQYMHAYPRIVHRDITSSNILLDSNFKAKI	453
Sbjct	312	KCSDTSRASLTWCQRISIAVDV+MGLQYMHAYPRIVHRDI SSNILLDSNFKAKI	371
Query	454	ANFSMARTFTNPMSKIDVFAFGVVLIELLTGRKAMTTKENGEVVMLWWDIWKIFDQEEN	513
Sbjct	372	ANFSMARTFTNP M KIDVFAFGVVLIELLTGRKAMTTKENGEVVMLWWDIWKIFDQEEN	431
Query	514	REERLRKWMDPKLNDNYPIDYALSLASLAVNCTADKSLSRPTIAEIVLSSLTQPSPAT	573
Sbjct	432	REERL+KWMDFKL++YYPIDYALSLASLAVNCTADKSLSR TAAEIVLSSLTQPSPAT	491
Query	574	LERSLTSSGLDVEATQIVTSISAR 597	
Sbjct	492	LERSLTSSGLDVEATQIVTSIAR 515	

>**emb|CAE02593.1|** SYM10 protein [Pisum sativum]
emb|CAE02594.1| SYM10 protein [Pisum sativum]

Length=594

Score = 870 bits (2247), Expect = 0.0, Method: Compositional matrix adjust.
 Identities = 437/600 (72%), Positives = 502/600 (83%), Gaps = 9/600 (1%)

Query	1	MAVFFVSLTLGAQILYVYVLMFF-TCIEAQSQQTNGTNFSCPSNSPPSCETYVTYISQSPN	59
Sbjct	1	MAVFF L + L++ LMFF T I AQ Q +GTNFSCP +SPPSCETYVTY ++SPN MAIFF--LPSSSHALMFVTNISAQPLQLSGTNFSCPVDSPPSCTYVTYFARSPN	58
Query	60	FLSLTSVSNIFDTSPLSIASRASNQHEEDKLIPGQVLLIPVTCGCTGNRSFANISYEINQ	119
Sbjct	59	FLSLT++S+IFD SPLSTA+ASN++ E+ KL+ GQVLLIPVTCGCT NR FAN +Y I FLSLTNISIDFDMSPLSIAKASNIEDEDKKLVEGQVLLIPVTCGCTRNYFANFTYTIKL	118
Query	120	GDSFYFVATTLYQNLTNWHAVMDLNPGLSQFTLPIGIQVVIPLFCKCP SKNQLDRGIKYL	179
Sbjct	119	GD+++ V+TT YQNLNTN+ + + NP LS LP I+VV+PLFCKCP SKNQL +GIK+L GDNYFIVSTTSYQNLNTNVEYEMENPNPLSPNLLPEI KVVPVLPFC KCP SKNQLSKGIKHL	178
Query	180	ITHVWQPNDNVSVFVSNKLGASPQDILSENNYQGNFTAASNLPLVLI PVTLLPDLIQSPSDG	239
Sbjct	179	ITVWQANDNVTRVSSKGASQVDMFTENN--QNTFAS TN PVI PTKLPVIDQPSNG	236
Query	240	RKHRIGLPV-IIIGISLGCTLLVVAISLKVCLMKMSLNRSASSAETADKLLSGVSGY	298
Sbjct	237	RK+ P IIIGISLG C VVV + LV V CLMKM LNR S AETADKLLSGVSGY RKNSTQKPAFIIGISLGCAFFVVVLTLSLVYVYCLKM KRLNR STS LAETADKLLSGVSGY	296
Query	299	VSKPTMYETGAI EATMNLSEQCKIGESVYKANIEGKVLAVKRFKEDVTEELKILQKVNH	358
Sbjct	297	VSKPTMY AI+EATMNLSE CKIGESVYKANI+G+VLAVK+ K+D +EELKILQKVNH	356
Query	359	GNLVKLMGVSSDNDGCNFVYVEYAENGSLEEWLFAKSCSETSNSRTSLTWCQRISIAVDV	418
Sbjct	357	GNLVKLMGVSSDNDGCNFVYVEYAENGSLDEWLSES-SKTSNSVVSLSWSQRITVAVDV	415
Query	419	SMGLQYMHAYPRIVHRDITSSNILLDSNFKAKIANFSMARTFTNPMSKIDVFAFGVV	478
Sbjct	416	++GLQYMHAY+HRDIT+SNI LLDSNFKAKIANFSMART TN MM KIDVFAFGVV AVGLQYMHAYTPRIHRDITSSNILLDSNFKAKIANFSMARTSTNSMMPKIDVFAFGVV	475
Query	479	LIELLTRKAMTTKENGEVVMLWWDIWKIFDQEENREERLRKWMDPKLNDNYPIDYALSL	538
Sbjct	476	LIELLTRKA ITT ENGEV V+W+LWWDIWKIFDQEENREERLRKWMDPKLNDNYPIDYALSL	535
Query	539	ASLAVNCTADKSLSRPTIAEIVLSSLTQPSPAT-TLERSLTSSGLDVEATQIVTSISAR	597
Sbjct	536	ASLAVNCTADKSLSRPTIAEIVLSSLTQPSPAT-TLERSLTSSGLDVEATQIVTSISAR ASLAVNCTADKSLSRPTIAEIVLSSLTQPSPAT-TLERSLTSSGLDVEATQIVTSISAR	594

>**gb|ADJ19110.1|** truncated Nod-factor receptor 5A [Glycine max]
 Length=501

Gene ID: 100498858 NFR5a | Nod-factor receptor 5A [Glycine max]
 (10 or fewer PubMed links)

Score = 866 bits (2238), Expect = 0.0, Method: Compositional matrix adjust.
 Identities = 434/501 (86%), Positives = 463/501 (92%), Gaps = 1/501 (0%)

Query	1	MAVFFVSLTLGAQILYVYVLMFF-TCIEAQSQQTNGTNFSCPSNSPPSCETYVTYISQSPN	59
Sbjct	1	MAVFF L L +QIL+V+M F T I AQSQQ N TNFSCPS+SPPSCETYVTYI+QSPN MAVFFPFLPLHSQILCLVIMLFSTNIVAQSQQDNRTNFSCPSDPPSCETYVTYIAQSPN	60
Query	60	FLSLTSVSNIFDTSPLSIASRASNQHEEDKLIPGQVLLIPVTCGCTGNRSFANISYEINQ	119
Sbjct	61	FLSLT++S+IFD SPLSTA+ASN++ +DKL+ QVLL+PVTCCGTGNRSFANISYEINQ FLSLTNISIDFDTSPLSIASRASNLEPMDDKLVQDQVLLPVTCCGTGNRSFANISYEINQ	120
Query	120	GDSFYFVATTLYQNLTNWHAVMDLNPGLSQFTLPIGIQVVIPLFCKCP SKNQLDRGIKYL	179
Sbjct	121	GDSFYFVATT Y+NLNTN AVMDLN P LS LPIGIQVW PLFCKCP SKNQLDRGIKYL GDSFYFVATT Y+NLNTN RAVMDLN P VS+K GASP+DI+SENNYQGNFTAA+NLPVLPVT LP L +SPSDG	180
Query	180	ITHVWQPNDNVSVFVSNKLGASPQDILSENNYQGNFTAASNLPLVLI PVTLLPDLIQSPSDG	239
Sbjct	181	ITVWQPGDNVSVLSDKFGASPEDIMSENNYQGNFTAANNLPLVLI PVTLPVLA RSPSDG	240
Query	240	RKHRIGLPV-IIIGISLGCTLLVVAISLKVCLMKMSLNRSASSAETADKLLSGVSGY	299
Sbjct	241	RK+ P IIIGISLGCTLLVVAISLKVCLMKMSLNRSASSAETADKLLSGVSGY RK+ P IIIGISLGCTLLVVAISLKVCLMKMSLNRSASSAETADKLLSGVSGY	300
Query	300	SKPTMYETGAI EATMNLSEQCKIGESVYKANIEGKVLAVKRFKEDVTEELKILQKVNHG	359
Sbjct	301	SKPTMYET AI+EATMNLSEQCKIGESVYKANIEGKVLAVKRFKEDVTEELKILQKVNHG SKPTMYET DAI+EATMNLSEQCKIGESVYKANIEGKVLAVKRFKEDVTEELKILQKVNHG	360
Query	360	NLVKLMGVSSDNDGCNFVYVEYAENGSLEEWLFAKSCSETSNSRTSLTWCQRISIAVDV	419
Sbjct	361	NLVKLMGVSSDNDGCNFVYVEYAENGSL+EWLF+KCS+TSNSR SLTW CQRIS+AVDV+	420
Query	420	MGLQYMHAYPRIVHRDITSSNILLDSNFKAKIANFSMARTFTNPMSKIDVFAFGVVL	479
Sbjct	421	MGLQYMHAYPRIVHRDITSSNILLDSNFKAKIANFSMARTFTNPMMPKIDVFAFGVVL MGLQYMHAYPRIVHRDITSSNILLDSNFKAKIANFSMARTFTNPMMPKIDVFAFGVVL	480
Query	480	IELLTRKAMTTKENGEVVML 500	

IELLTGRKAMTTKENGEVVML
 Sbjct 481 IELLTGRKAMTTKENGEVVML 501

>emb|CAE02595.1| SYM10 protein [Pisum sativum]
 emb|CAE02596.1| SYM10 protein [Pisum sativum]
 gb|ADB45277.1| Nod factor recognition protein [Pisum sativum]
 Length=594

Score = 865 bits (2236), Expect = 0.0, Method: Compositional matrix adjust.
 Identities = 435/600 (72%), Positives = 501/600 (83%), Gaps = 9/600 (1%)

Query 1 MAVFFVSLTGAQI LYVVL MFF-TCIEAQSQQTNGTNFSCPSNSPPSCETYVTYISQSPN 59
 Sbjct 1 MAFF+ L + L++ LMFF T I AQ Q +GTNESCP +SPPSCETYVTY ++SPN 58

Query 60 FLSLTSVSNIFDTSPLSIARASN LQHEEDKLIPGQVLLIPVTCGCTGNRSFANISYEINQ 119
 Sbjct 59 FLSLT++S+IFD SPLSIA+ASN++ E+ KLT GQVLLIPVTCGCT NR FAN +Y I 118

Query 120 GDSFYFVATTLYQNLTNWHAVMMDLNPGLSQFTLPIGIQVVIPLFCKCPSKNQLDRGIKYL 179
 Sbjct 119 GDNYFIVSTTSQYQNLTNYVEMENFNPNLSPNLLPPEIKV VVPLFCKCPSKNQLSKGIKHL 178

Query 180 ITHWQOPNDNVFSVNKLGASPQDILSENNYGNFTAASNLPLVLPVTLPLDIQSPSDG 239
 Sbjct 179 ITYWQANDNVTRVSSKGASQVDMFTENN--QNFTASTNVPLIPVTKLPVIDQPSSNG 236

Query 240 RKHRIGLPV-IIGISLGCTLLVVVSAILLCVCCCLKMKS LNRSSAETADKLLSGVGSGY 298
 Sbjct 237 RKNSTQKPAFIIGISLGCAFFVVVLTLSLVYVYCLMKRNLNRSTAETADKLLSGVGSGY 296

Query 299 VSKPTMYETGAI EATMNL SEQCKIGESVYKANIEGKVLA VKRKFEDVTEELKILQKVNH 358
 Sbjct 297 VSKPTMYEMA DAIMETMNL SEQCKIGESVYKANIDGRVLAVKKIKKDASEELKILQKVNH 356

Query 359 GN LKLMGVSSDNDGNCFVVYEAENG SLEEW LFAKSCSETNSRSTS LTWCORISIAVDV 418
 Sbjct 357 GN LKLMGVSSDN+GNCF+VYEAENGSL+EWF++ S+TSNS SLTW QR+ +AVDV 415

Query 419 SMGLQYMHEAYPRVHDITSSNILLDSNFKA KIANFSMARTFTNPMM SKIDVFAFGVV 478
 Sbjct 416 AVG LQYMHEHTYPRIIHRDITTSNILLDSNFKA KIANFSMARTSTNSMMPKIDVFAFGVV 475

Query 479 LIELLTGRKAMTTKENGEVVMLWKDIKFDQEENREERLRKWM DP KLDNYY PIDYALSL 538
 Sbjct 476 LIELLTGKAITTMENGEVVILWKDFW KIFDLEGNREESLRKWM DP KLENFYPIDNALSL 535

Query 539 ASLAVNCTADKSLSRPTIAEIVL SLSLTQPS -TLERSLTSSGLDVEATQIVTSIAR 597
 Sbjct 536 ASLAVNCTADKSLSRPSIAEIVLCSLLNQSSSEPMLRSIT-SGLDVEATHVVTISIAR 594

>emb|CAE02597.1| Nod-factor receptor 5 [Lotus japonicus]
 emb|CAE02598.1| Nod-factor receptor 5 [Lotus japonicus]
 Length=595

Gene ID: 100034751 NFR5 | Nod-factor receptor 5 [Lotus japonicus]
 (10 or fewer PubMed links)

Score = 862 bits (2227), Expect = 0.0, Method: Compositional matrix adjust.
 Identities = 432/601 (71%), Positives = 502/601 (83%), Gaps = 10/601 (1%)

Query 1 MAVFFVSLTGAQI LYVVL MFF-TCIEAQSQQTNGTNFSCPSNSPPSCETYVTYISQSPN 59
 Sbjct 1 MAVFF+ LT G+ L++ L I A+S++ +G+FSCP +SPPSCETYVTY +QSPN 58

Query 60 FLSLTSVSNIFDTSPLSIARASN LQHEEDKLIPGQVLLIPVTCGCTGNRSFANISYEINQ 119
 Sbjct 59 FLSLT++S+IFD SPLSIA+ASN++ E+ KLT GQVLLIPVTCGCT NR FAN +Y I 118

Query 120 GDSFYFVATTLYQNLTNWHAVMMDLNPGLSQFTLPIGIQVVIPLFCKCPSKNQLDRGIKYL 179
 Sbjct 119 GDSYDFVATTLYENLTNWIVASNPVGVPYLLPERVKVVFPLFCRCPSKNQLNKGIQYL 178

Query 180 ITHWQOPNDNVFSVNKLGASPQDILSENNYGNFTAASNLPLVLPVTLPLDIQSPSDG 239
 Sbjct 179 ITYWQPNNDNVFSVLSAKF GASPA DILTENRYGQDFTAA TNPLTIPVTLPELTQPSNG 238

Query 240 RKHRIGLPV-IIGISLGCTLLVVVSAILLCVCCCLKMKS LNRSSAETADKLLSGVGSGY 299
 Sbjct 239 RKKSIHLLVILGITLGCTLLTAVLTGTLVYVYCRKKALNRTASSAETADKLLSGVGSGY 298

Query 300 SKPTMYETGAI EATMNL SEQCKIGESVYKANIEGKVLA VKRKF-EVTEELKILQKVNH 358
 Sbjct 299 SKPNVYEIDEIMEATKDSDECKVGESVYKANIEGRVVA VKKIKEGGANEELKILQKVNH 358

Query 359 GN LKLMGVSSDNDGNCFVVYEAENG SLEEW LFAKSCSETNSRSTS LTWCORISIAVDV 418
 Sbjct 359 GN LKLMGVSS DGNCF+VYEAENGSL+EWF++ S+ SLTW QRISIAVDV 414

Query 419 SMGLQYMHEAYPRVHDITSSNILLDSNFKA KIANFSMARTFTNPMM SKIDVFAFGVV 478
 Sbjct 415 AVG LQYMHEHTYPRIIHRDITTSNILLDSNFKA KIANFAMARTSTNPMPKIDVFAFGVV 474

Query 479 LIELLTGRKAMTTKENGEVVMLWKDIKFDQEENREERLRKWM DP KLDNYY PIDYALSL 538
 Sbjct 475 LIELLTGRKAMTTKENGEVVMLWKD+W+IFD EENREER+RKWMDP L++Y ID ALSL 534

Query 539 ASLAVNCTADKSLSRPTIAEIVL SLSLTQPS -ATLERSLTSSGLDVE-ATQIVTSIAR 596
 Sbjct 535 ASLAVNCTADKSLSRPSIAEIVLCSLLNQSSSEPMLRSIT-SGLDVEATHVVTISIAR 594

Query 597 R 597
 Sbjct 595 R 595

>**gb|ABF50224.1| Nod factor perception protein [Medicago truncatula]**
Length=595

Score = 839 bits (2168), Expect = 0.0, Method: Compositional matrix adjust.
Identities = 422/599 (70%), Positives = 493/599 (82%), Gaps = 6/599 (1%)

Query 1	MAVFFVSLTLGAQILYVVLMLFFTICIEAQSQQTNGTNFSCPSNSPPSCETYVTYISQSPNF	60
Sbjct 1	M ⁺ FF ⁺ + A L ⁺⁺ L F T I A Q ⁺ + TNF+CP ⁺ SPPSCETYV Y ⁺ QSPNF	60
Query 61	LSLTSVSNIFDTSPLSIARASNLQHEEDKLIPGQVLLI PVTCCCTGNRSFANISYEINQ	120
Sbjct 61	LSLT ⁺⁺ +S ⁺ I ⁺ F ⁺ SPL IA ⁺ ASN ⁺⁺ E ⁺ KLIP Q ⁺⁺ L ⁺ PVTCCGT N SFAN ⁺⁺ Y I QG	120
Query 121	D ⁺ S ⁺ F ⁺ + T YQNLTN ⁺⁺ + NP LS LP ⁺ +V +PLFKCPSKNQL ⁺⁺ GIKYLI	180
Sbjct 121	DNF ⁺ F ⁺ I ⁺ S ⁺ T ⁺ SYQNLTN ⁺⁺ LEFKNFPNLSPTLPLDTKVSVPFLFKCPSKNQLNKIGIKYLI	180
Query 181	THWQPNDNVSVFSVSNKLGASPQDILSENNYQGNFTAASNLPVLI PVTLLPDLIQSPSDGR	240
Sbjct 181	T ⁺ VWQ NDNV ⁺ VS ⁺ K GAS ⁺⁺ L ⁺⁺ NN ⁺ NFTA ⁺⁺ N VLPVT LP L Q S ⁺ GR	238
Query 241	KHRI-GLPVIIGISLGCTLLVVSAILLVCVCLKMKSLSNRSASSAETADKLLSGVSGYV	299
Sbjct 239	K ⁺ L ⁺ I ⁺ G ⁺ ISLG ⁺⁺ V + LV C ⁺ CLKMK LNRS SS ⁺ ETADKLLSGVSGYV	298
Query 300	SKPTMYETGAI ⁺ EATMNLSEQCKI ⁺ GESVYKANIEGKVLA ⁺ KRFKEDVTEELKILQKVNHG	359
Sbjct 299	SKPTMYE AI ⁺ E T NLS ⁺ CKIGESVYKANI ⁺ G ⁺ VLA ⁺ V K ⁺ D ⁺ EE ⁺ ELKILQKVNHG	358
Query 360	NLVKLMGVSSNDGNCF ⁺ VYE ⁺ ENG ⁺ SL ⁺⁺ WLF ⁺⁺ S S ⁺ TSNS SLTW QRI ⁺ IA ⁺ DV ⁺	419
Sbjct 359	NLVKLMGVSSNDGNCF ⁺ L ⁺ VYE ⁺ ENG ⁺ SL ⁺⁺ WLF ⁺⁺ S S ⁺ TSNS SVS ⁺ LTWSQRITIAMDVA	417
Query 420	MGLQYMHEAYPRIHARDITSSNILLDSNFKA ⁺ KIANFSMARTFTNPMMSKIDVFAFGVVL	479
Sbjct 418	+GLOYMHEH YPRI ⁺ HARDIT ⁺⁺ SNILLDSNFKA ⁺ KIANFSMARTFTNSMMPKIDVFAFGVVL	477
Query 480	IELLTGRKAMTTKENGEVVMILWKDIWKFIDQEEENREERL ⁺ RKWM ⁺ DPKLDNYYPIDYALSLA	539
Sbjct 478	IELLTG ⁺ KAMTTKENGEVVM ⁺ LWKF WKFID E NREERL ⁺ RKWM ⁺ DPKLDNYYPIDYALSLA	537
Query 540	SLAVNCTADKSLSRPTIAEIVLSSLTQPSA-TLERSLTSSGLDVEATQIVTSISAR	597
Sbjct 538	SLAVNCTADKSLSRPTIAEIVLSSLINQPSSEPLERSLT-SGLDAEATHVVT ⁺ SVIAR	595

>**emb|CAO02956.1| LysM-domain containing receptor-like kinase [Medicago truncatula]**
var. truncatula
Length=498

Score = 740 bits (1910), Expect = 0.0, Method: Compositional matrix adjust.
Identities = 358/497 (72%), Positives = 420/497 (84%), Gaps = 4/497 (0%)

Query 45	PSCETYV ⁺ TYISQSPNFLSLTSVSNIFDTSP ⁺ LSIARASNLQHEEDKLIPGQVLLI PVT ⁺ TCGC	104
Sbjct 4	PSCETYV Y ⁺ QSPNFLSL ⁺⁺ S ⁺ I ⁺ F ⁺ SPL IA ⁺ ASN ⁺⁺ E ⁺ KLIP Q ⁺⁺ L ⁺ PVT ⁺ CGC	63
Query 105	TGNRSFANISYEINQGDSFYFVATTLYQNLTNWHA ⁺ MDLNPGLSQFTLPIGIQVVIPLFC	164
Sbjct 64	T N SFAN ⁺⁺ Y I QGD ⁺⁺ F ⁺⁺ + T YQNLTN ⁺⁺ + NP LS LP ⁺ +V +PLFC	123
Query 165	KCPSKNQLDRGIKYLITHVWQPNDNVSVFSVSNKLGASPQDILS ⁺⁺ ENNYQGNFTAASNL ⁺⁺ PLVLI	224
Sbjct 124	KCPSKNQLDRGIKYLITHVWQDN ⁺⁺ DNVTLVSSKG ⁺ ASQVEMLAENN ⁺⁺ NFTASTNR ⁺⁺ SVLI	181
Query 225	PVTLLPDLIQSPS ⁺ GRKHRI-GLPVIIGISLGCTLLVVSAILLVCVCLKMKSLSNRSAS	283
Sbjct 182	PVT LP L Q S ⁺ GRK L ⁺ I ⁺ G ⁺ ISLG ⁺⁺ V + LV V CLKMK LNRS S	241
Query 284	SAETADKLLSGVGSGYVSKPTMYETGAI ⁺ EATMNLSEQCKI ⁺ GESVYKANIEGKVLA ⁺ KRFK	343
Sbjct 242	S ⁺ SETADKLLSGVGSGYVSKPTMYE AI ⁺ E TMNL ⁺ S CKIGESVYKANI ⁺ G ⁺ VLA ⁺ V K	301
Query 344	EDVTEELKILQKVNHGNL ⁺ VKL ⁺ MGVSSNDGNCFV ⁺ YYE ⁺ ENG ⁺ SL ⁺⁺ WLF ⁺⁺ S S ⁺ TSNS	403
Sbjct 302	KDASEELKILQKVNHGNL ⁺ VKL ⁺ MGVSSNDGNCF ⁺ LVYE ⁺ ENG ⁺ SL ⁺⁺ WLF ⁺⁺ S SKTSNSV	360
Query 404	TSLTW ⁺ CQRISIAV ⁺ DVSMGLQYMHEAYPRIHARDITSSNILLDSNFKA ⁺ KIANFSMARTFT	463
Sbjct 361	S ⁺ TSNS QRISIAV ⁺ DV ⁺ +GLQYMHEH YPRI ⁺ HARDIT ⁺⁺ SNILLDSNFKA ⁺ KIANFSMARTFT	420
Query 464	NPMMSKIDVFAFGVVLIELLTGRKAMTTKENGEVVMILWKDIWKFIDQEEENREERL ⁺ RKWM ⁺ D	523
Sbjct 421	N MM KIDVFAFGVVLIELLTG ⁺ KAMTTKENGEVVM ⁺ LWKF WKFID E NREERL ⁺ RKWM ⁺ DLEG ⁺ NREERL ⁺ RKWM ⁺ D	480
Query 524	PKLDNYYPIDYALSLAS	540
Sbjct 481	PKL ⁺⁺ Y ⁺ PID ALS ⁺ AS	497

>**emb|CAO02958.1| LysM-domain containing receptor-like kinase [Medicago truncatula]**
var. truncatula
Length=492

Score = 733 bits (1892), Expect = 0.0, Method: Compositional matrix adjust.
Identities = 355/494 (71%), Positives = 417/494 (84%), Gaps = 4/494 (0%)

Query 48	ETYYV ⁺ YISQSPNFLSLTSVSNIFDTSP ⁺ LSIARASNLQHEEDKLIPGQVLLI PVT ⁺ CGCTGN	107
Sbjct 1	ETYYV Y ⁺ QSPNFLSL ⁺⁺ S ⁺ I ⁺ F ⁺ SPL IA ⁺ ASN ⁺⁺ E ⁺ KLIP Q ⁺⁺ L ⁺ PVT ⁺ CGCTGN	60
Query 108	RSFANISYEINQGDSFYFVATTLYQNLTNWHA ⁺ MDLNPGLSQFTLPIGIQVVIPLFC	167
Sbjct 61	SFAN ⁺⁺ Y I QGD ⁺⁺ F ⁺⁺ + T YQNLTN ⁺⁺ + NP LS LP ⁺ +V +PLFC	120
Query 168	SKNQLDRGIKYLITHVWQPNDNVSVFSVSNKLGASPQDILSENNYQGNFTAASNL ⁺⁺ PLVLI PVT	227

Sbjct 121 SKNQL++GIKYLLIT+VWQ NDNW+ VS+K GAS ++L+ENN+ NFTA++N VLIPVT
 Sbjct 121 SKNQLNKGKIKYLITYWQNDNDNTLVSSKGASQVEMLAENNHH--NFTASTNRSLIPVT 178

Query 228 LLPDLIQSPSDGRKHRI-GLPVIIGISLGCTLLVVVSAILLCVCCCLKMKSLNRSASSAE
 LP L Q S+GRK L +IIGISLG ++V + LV V CLKMK LNRS SS+E 286

Sbjct 179 SLPKLDQPSNSGRKSSSQNLALIIGISLSAFFILVLTSLVYVYCLMKRKLNRSTSSSE 238

Query 287 TADKLLSGVGSGYVSKPTMYETGAILEATMNLSEQCKIGESVYKANIEGKVLAVKRFKEDV
 TADKLLSGVGSGYVSKPTMYE AI+E TMNL+S CKIGESVYKANI+G+VLAVK+ K+D 346

Sbjct 239 TADKLLSGVGSGYVSKPTMYEIDAIMEGTMNLSDNCCKIGESVYKANIDGRVLAVKKIKKDA 298

Query 347 TEELKILQKVNHGNLVKLMGVSSNDGNCFVYVEYAENGSLLEWLFAKSCSETNSRTSL
 +TEELKILQKVNHGNLVKLMGVSSNDGNCF+VYEYAENGSLLEWLFL+S S+TSNS SL 406

Sbjct 299 SEELKILQKVNHGNLVKLMGVSSNDGNCFLVYVEYAENGSLLEWLFSSES-SKTSNSVVSL 357

Query 407 TWCRISIAVDVSMGLQYMHEAYPRIHARDITSSNILLDSNEAKIANFSMARTFTNPM
 TW QRI+IA+DV++GLQYMHEH YPRI+HRDIT+SNILL SNFKAKIANF MART TN M 466

Sbjct 358 TWSQRITIAMDVAIGLQYMHEHTYPRIHARDITTSNILLGSNFKAKIANFGMARTSTNSM 417

Query 467 MSKIDVFAGVVILIETGRKAMTTKENGEVVMLWKDIWKIFDQEENREERLRKWMDPKL
 M KIDVFAGVVILIETLTGKAMTTKENGEVV+LWKD WKIFD E NREERLRKWMDPKL 526

Sbjct 418 MPKIDVFAGVVILIETLTGKAMTTKENGEVVLWKDFWKIFDLEGNRERLRKWMDPKL 477

Query 527 DNYYPIDYALSLAS 540
 +-+YPID ALS+AS

Sbjct 478 ESFYPIDNALSMAS 491

>**emb|CAO02933.1|** LysM-domain containing receptor-like kinase [Medicago truncatula
 var. truncatula]
emb|CAO02934.1| LysM-domain containing receptor-like kinase [Medicago truncatula
 var. truncatula]
emb|CAO02935.1| LysM-domain containing receptor-like kinase [Medicago truncatula
 var. truncatula]

10 more sequence titles

emb|CAO02938.1| LysM-domain containing receptor-like kinase [Medicago truncatula
 var. truncatula]
emb|CAO02939.1| LysM-domain containing receptor-like kinase [Medicago truncatula
 var. truncatula]
emb|CAO02952.1| LysM-domain containing receptor-like kinase [Medicago truncatula
 var. longicauleata]
emb|CAO02955.1| LysM-domain containing receptor-like kinase [Medicago truncatula
 var. truncatula]
emb|CAO02957.1| LysM-domain containing receptor-like kinase [Medicago truncatula
 var. truncatula]
emb|CAO02959.1| LysM-domain containing receptor-like kinase [Medicago truncatula
 var. truncatula]
emb|CAO02967.1| LysM-domain containing receptor-like kinase [Medicago truncatula
 var. truncatula]
emb|CAO02971.1| LysM-domain containing receptor-like kinase [Medicago truncatula
 var. truncatula]
emb|CAO02972.1| LysM-domain containing receptor-like kinase [Medicago truncatula
 var. truncatula]
emb|CAO02973.1| LysM-domain containing receptor-like kinase [Medicago truncatula
 var. truncatula]

Length=487

Score = 725 bits (1871), Expect = 0.0, Method: Compositional matrix adjust.
 Identities = 351/489 (71%), Positives = 413/489 (84%), Gaps = 4/489 (0%)

Query 53 YISQSPNFLSLSVSNIFDTSPSLIARASNLLQHEEDKLIPGQVLLIPVTCGCTGNRSFAN 112
 Y +QSPNFLSL++S+IF+ SPL IA+ASN++ E+ KLIP Q+LL+PVTGCT N SFAN
 Sbjct 1 YRAQSPNFLSLSNISDIFNLSPRLIAKASNIEADEDKKLIPDQLLVPVTCGCTKNHSFAN 60

Query 113 ISYEINQGDSFYFVATTLYQNLNTNWHAVMIDLNGLSQFTLPIGIVQVVIPLFCCKPSKNQL 172
 I+Y I QGD+F+ ++ T YQNLNT+ + NP LS LP+ +V +PLFCCKPSKNQL
 Sbjct 61 ITYSIKQGDNNFILSITSYQNLNTYLEFKNFPNLSPTLLPLDKVSVPLFCCKPSKNQL 120

Query 173 DRGIKYLLITHWQPNDNVSFVSNKLGASPQDILSENNEYQGNFTAASNLPLVLPVTLLPDL 232
 ++GIKYLLIT+WQ WDNV+ VS+T GAS ++L+ENN+ NFTA++N VLIPVT LP L
 Sbjct 121 NKGIKYLLITYWQDNDNTVLSKSKFGASQVEMLAENNHH--NFTASTNRSLIPVTSPLPKL 178

Query 233 IQSPSDGRKHRI-GLPVIIGISLGCTLLVVVSAILLCVCCCLKMKSLNRSASSAETADKL 291
 Q S+GRK L +IIGISLG ++V + LV V CLKMK LNRS SS+ETADKL
 Sbjct 179 DQPSSNSGRKSSSQNLALIIGISLSAFFILVLTSLVYVYCLMKRKLNRSTSSSETADKL 238

Query 292 LSGVSGYVSKPTMYETGAILEATMNLSEQCKIGESVYKANIEGKVLAVKRFKEDVTEELK 351
 LSGVSGYVSKPTMYE AI+E TMNL+S CKIGESVYKANI+G+VLAVK+ K+D +EELK
 Sbjct 239 LSGVSGYVSKPTMYEIDAIMEGTMNLSDNCCKIGESVYKANIDGRVLAVKKIKKDAEELK 298

Query 352 ILQKVNHGNLVKLMGVSSNDGNCFVYVEYAENGSLLEWLFAKSCSETNSRTSLTWCQR 411
 ILQKVNHGNLVKLMGVSSNDGNCF+VYEYAENGSLLEWLFL+S S+TSNS SLTW QR
 Sbjct 299 ILQKVNHGNLVKLMGVSSNDGNCFLVYVEYAENGSLLEWLFSSES-SKTSNSVSVSLTWSQR 357

Query 412 ISIAVDVSMGLQYMHEAYPRIHARDITSSNILLDSNFKAKIANFSMARTFTNPMMSKID 471
 I+IA+DV++GLQYMHEH YPRI+HRDIT+SNILL SNFKAKIANF MART TN MM KID
 Sbjct 358 ITIAMDVAIGLQYMHEHTYPRIHARDITTSNILLGSNFKAKIANFGMARTSTNSMMPKID 417

Query 472 VFAGVVILIETLTGKAMTTKENGEVVMLWKDIWKIFDQEENREERLRKWMDPKLNYYP 531
 VFAGVVILIETLTGKAMTTKENGEVV+LWKD WKIFD E NREERLRKWMDPKL++YYP
 Sbjct 418 VFAGVVILIETLTGKAMTTKENGEVVLWKDFWKIFDLEGNRERLRKWMDPKLESFYP 477

Query 532 IDYALSLAS 540
 ID ALS+AS
 Sbjct 478 IDNALSMAS 486

>**emb|CAO02940.1|** LysM-domain containing receptor-like kinase [Medicago truncatula
 var. truncatula]
 Length=487

Score = 723 bits (1866), Expect = 0.0, Method: Compositional matrix adjust.
 Identities = 351/489 (71%), Positives = 412/489 (84%), Gaps = 4/489 (0%)

Query 53 YISQSPNFLSLSVSNIFDTSPSLIARASNLLQHEEDKLIPGQVLLIPVTCGCTGNRSFAN 112
 Y +QSPNFLSL++S+IF+ SPL IA+ASN++ E+ KLIP Q+LL+PVTGCT N SFAN
 Sbjct 1 YRAQSPNFLSLSNISDIFNLSPRLIAKASNIEADEDKKLIPDQLLVPVTCGCTKNHSFAN 60

Query 113 ISYEINQGDSFYFVATTLYQNLNTNWAVMDLNPGLSQFTLPIGIQVVIPLFCKCPSKNQL 172
 Sbjct 61 ITYSIKQGDNFFILSITSYQNLNTYLEFKNFNPNLSPTLLPLDTKVSPLFCKCPSKNQL 120

Query 173 DRGIKYLITHWQPNDNVSFVSNKLGASPQDILSENNYQGNFTAASNLPVLIPTVLLPDL 232
 Sbjct 121 NKGIKYLITYVWQNDNDNVTLVSSKFGASQVEMLAENNHH--NFTASTNRSVLIPVTSPLKL 178

Query 233 IQSPSDGRKHRI-GLPVIIIGISLGCTLLVVSAIALLVCVCCMKSLNRSASSAETADKL 291
 Sbjct 179 DQPSSNGRKSSSQNLALIIIGISLGSAFFILVLTSLVYVYCLMKRRLNRSTSSSETADKL 238

Query 292 LSGVSGYVSKPTMYETGAILEATMNLSEQCKIGESVYKANIEGKVLAVKRFKEDVTEELK 351
 Sbjct 239 LSGVSGYVSKPTMYEIDAIMEGTNLSDNCKIGESVYKANIDGRVLAVKKIKKDASEELK 298

Query 352 ILQKVNHGNLVKLMGVSSNDGNCFCVYEAENGSLLEEWLF+S+TSNS SLTW QR 411
 Sbjct 299 ILQKVNHGNLVKLMGVSSNDGNCFLVYEAENGSLLEEWLFSESW-KTSNSVSVSLTWSQR 357

Query 412 ISIAVDVSMGLQYMHEHAYPRIHRDITSSNILLDSNFKAKIANFSMARTFTNPMMSKID 471
 Sbjct 358 ITIAMDVAILGLQYMHEHTYPRIIHRDITTSNILLGSNFKAKIANFGMARTSTNSMMPKID 417

Query 472 VFAFGVVLIELLTGRKAMTTKENGEVVMWLWDIWKIFDQEENREERLRKWMDPKLDNYP 531
 Sbjct 418 VFAFGVVLIELLTGKAMTTKENGEVVLWKFWDKIFDLEGNRERLRKWMDPKLESFYP 477

Query 532 IDYALSLAS 540
 Sbjct 478 IDNALSLAS 486

>**emb|CAO02951.1|** LysM-domain containing receptor-like kinase [Medicago truncatula]
 var. truncatula]
 Length=487

Score = 723 bits (1866), Expect = 0.0, Method: Compositional matrix adjust.
 Identities = 351/489 (71%), Positives = 412/489 (84%), Gaps = 4/489 (0%)

Query 53 YISQSPNFLSLSVSNIQFDTSPLSIARASNQHEEDDKLIPGQVLLIPVTCGCTGNRSFAN 112
 Sbjct 1 YRAQSPNFLSLSNISDIFNLSPLRIAKASNIEADKKLIPDQLLVPVTCGCTKNHSFAN 60

Query 113 ISYEINQGDSFYFVATTLYQNLNTNWAVMDLNPGLSQFTLPIGIQVVIPLFCKCPSKNQL 172
 Sbjct 61 ITYSIKQGDNFFILSITSYQNLNTYLEFKNFNPNLSPTLLPLDTKVSPLFCKCPSKNQL 120

Query 173 DRGIKYLITHWQPNDNVSFVSNKLGASPQDILSENNYQGNFTAASNLPVLIPTVLLPDL 232
 Sbjct 121 NKGIKYLITYVWQNDNDNVTLVSSKFGASQVEMLAENNHH--NFTASTNRSVLIPVTSPLKL 178

Query 233 IQSPSDGRKHRI-GLPVIIIGISLGCTLLVVSAIALLVCVCCMKSLNRSASSAETADKL 291
 Sbjct 179 DQPSSNGRKSSSQNLALIIIGISLGSAFFILVLTSLVYVYCLMKRRLNRSTSSSETADKL 238

Query 292 LSGVSGYVSKPTMYETGAILEATMNLSEQCKIGESVYKANIEGKVLAVKRFKEDVTEELK 351
 Sbjct 239 LSGVSGYVSKPTMYEIDAIMEGTNLSDNCKIGESVYKANIDGRVLAVKKIKKDASEELK 298

Query 352 ILQKVNHGNLVKLMGVSSNDGNCFCVYEAENGSLLEEWLF+S+TSNS SLTW QR 411
 Sbjct 299 ILQKVNHGNLVKLMGVSSNDGNCFLVYEAENGSLLEEWLFSESW-KTSNSVSVSLTWSQR 357

Query 412 ISIAVDVSMGLQYMHEHAYPRIHRDITSSNILLDSNFKAKIANFSMARTFTNPMMSKID 471
 Sbjct 358 ITIAMDVAILGLQYMHEHTYPRIIHRDITTSNILLGSNFKAKIANFGMARTSTNSMMPKID 417

Query 472 VFAFGVVLIELLTGRKAMTTKENGEVVMWLWDIWKIFDQEENREERLRKWMDPKLDNYP 531
 Sbjct 418 VFAFGVVLIELLTGKAMTTKENGEVVLWKFWDKIFDLEGNRERLRKWMDPKLESFYP 477

Query 532 IDYALSLAS 540
 Sbjct 478 IDNALSLAS 486

>**emb|CAO02941.1|** LysM-domain containing receptor-like kinase [Medicago truncatula]
 var. truncatula]
emb|CAO02970.1| LysM-domain containing receptor-like kinase [Medicago truncatula]
 var. truncatula]
 Length=487

Score = 722 bits (1863), Expect = 0.0, Method: Compositional matrix adjust.
 Identities = 350/489 (71%), Positives = 412/489 (84%), Gaps = 4/489 (0%)

Query 53 YISQSPNFLSLSVSNIQFDTSPLSIARASNQHEEDDKLIPGQVLLIPVTCGCTGNRSFAN 112
 Sbjct 1 YRAQSPNFLSLSNISDIFNLSPLRIAKASNIEADKKLIPDQLLVPVTCGCTKNHSFAN 60

Query 113 ISYEINQGDSFYFVATTLYQNLNTNWAVMDLNPGLSQFTLPIGIQVVIPLFCKCPSKNQL 172
 Sbjct 61 ITYSIKQGDNFFILSITSYQNLNTYLEFKNFNPNLSPTLLPLDTKVSPLFCKCPSKNQL 120

Query 173 DRGIKYLITHWQPNDNVSFVSNKLGASPQDILSENNYQGNFTAASNLPVLIPTVLLPDL 232
 Sbjct 121 NKGIKYLITYVWQNDNDNVTLVSSKFGASQVEMLAENNHH--NFTASTNRSVLIPVTSPLKL 178

Query 233 IQSPSDGRKHRI-GLPVIIIGISLGCTLLVVSAIALLVCVCCMKSLNRSASSAETADKL 291
 Sbjct 179 DQPSSNGRKSSSQNLALIIIGISLGSAFFILVLTSLVYVYCLMKRRLNRSTSSSETADKL 238

Query 292 LSGVSGYVSKPTMYETGAILEATMNLSEQCKIGESVYKANIEGKVLAVKRFKEDVTEELK 351
 Sbjct 239 LSGVSGYVSKPTMYEIDAIMEGTNLSDNCKIGESVYKANIDGRVLAVKKIKKDASEELK 298

Query 352 ILQKVNHGNLVKLMGVSSNDGNCFCVYEAENGSLLEEWLF+S+TSNS SLTW QR 411

Sbjct	299	ILQKVNHNGLVKLMLGVSSDNDGNCF+VYEYAENGSLLEELWF++S S+TSNS SLTW QR ILQKVNHNGLVKLMLGVSSDNDGNCFLVYEAENGSLLEELWFSES-SKTSNSVSVSLTWSQR	357
Query	412	ISIAVDVSMGLQYMHEHAYPRIVRHDITSSNILLDSNFKAKIANFSMARTFTNPMMSKID I+IA+DV++GLQYMHEH YPRI+HRDIT+SNIIL SNFKAKIANF MART TN MM KID	471
Sbjct	358	ITIAMDVAIGLQYMHEHTYPRIIHRDITTSNILLGSNFKAKIANFGMARTSTNSMMPKID	417
Query	472	VFAFGVVLIELLTGRKAMTTKENGEVVMLWWDKIWFIDQEEENREERLKWMDPKLDNYYP VFAFGVVLIELLTG+KAMTTKENGEVV+LWWD WKIFD E NEERERLKWMDPKL++YP	531
Sbjct	418	VFAFGVVLIELLTGKAMTTKENGEVVLWWDKFWKIFDLEGNRERERLKWMDPKLESFYP	477
Query	532	IDYALSLAS 540	
Sbjct	478	ID ALSLAS	486

>emb|CAO02966.1| LysM-domain containing receptor-like kinase [Medicago tornata]
Length=487

Score = 718 bits (1853), Expect = 0.0, Method: Compositional matrix adjust.
Identities = 349/489 (71%), Positives = 411/489 (84%), Gaps = 4/489 (0%)

Query	53	YISQSPNPLSLTSVSNIFDTSPSLIARASNLLQHEEDKLIPGQVLLIPVTCGCTGNRSFAN Y +QSPPNPLSL++S++IF+ SPL IA+ASN++ E + KLIP Q+LL+PVTGCT N SFAN	112
Sbjct	1	YRAQSPNPLSLNSNISDFNLSPRLIAKASNIEADKKLIPDQLLVPVTCGCTKNHSFAN	60
Query	113	ISYEINQGDSFYFVATTLYQNLTNWAVMDLNPGSQFTLPIGIQVVIPLFKCPSKNQL I+Y I GD+F+ ++ T YQNLTN+ + NP LS LP+ +V +PLFKCPSKNQL	172
Sbjct	61	ITYSIKLGDNFFILSITSYQNLTNYLEFKNFNPNLSPTLPLDTKVSVPFLFKCPSKNQL	120
Query	173	DRGIKYLITHWQPNDNNSFVSNKLGASPQDILSENNYQGQNFTAASNLPVLIPTVLLPDL ++GIKYLID++VWO NDNV+ VS+K GAS ++L+ENN+ NFTA++N VLIPTV LP L	232
Sbjct	121	NKGIKYLITYVWQDNDNVTLVSSKFGASQVEMLAENN--NFTASTNRNSVLIPTVSLPKL	178
Query	233	IQSPSDGRKHRI-GLPVIIGISLGCTLLVVSAIILVCVCLMKMSLNRASSAETADKL Q S+GRK L +IIGISLG ++V + LV V CLMK LNRS SS+ETADKL	291
Sbjct	179	DQPPSSNGRKSSQNLALIIGISLGAFFILVLTSLVYVYCLMKRKLNRSTSSSETADKL	238
Query	292	LSGVSGYVSKPTMYETGAILEATMNLSEQCKIGESVYKANIEGKVLAVKRFKEDVTEELK LSGVSGYVSKPTMYE AI+E TMNL+S CKIGESVYKANI+G+VLAVK+ K+D +EELK	351
Sbjct	239	LSGVSGYVSKPTMYEIDAIMEGTMLSDNCKIGESVYKANIDGRVLAVVKIKKDAEELK	298
Query	352	ILQKVNHNGLVKLMLGVSSDNDGNCF+VYEYAENGSLLEELWF++S S+TSNS SL+W QR ILQKVNHNGLVKLMLGVSSDNDGNCFLVYEAENGSLLEELWFSES-SKTSNSVSVSLWSQR	411
Sbjct	299	ILQKVNHNGLVKLMLGVSSDNDGNCFLVYEAENGSLLEELWFSES-SKTSNSVSVSLWSQR	357
Query	412	ISIAVDVSMGLQYMHEHAYPRIVRHDITSSNILLDSNFKAKIANFSMARTFTNPMMSKID I+IA+DV++GLQYMHEH YPRI+HRDIT+SNIIL SNFKAKIANF MART TN MM KID	471
Sbjct	358	ITIAMDVAIGLQYMHEHTYPRIIHRDITTSNILLGSNFKAKIANFGMARTSTNSMMPKID	417
Query	472	VFAFGVVLIELLTGRKAMTTKENGEVVMLWWDKIWFIDQEEENREERLKWMDPKLDNYYP VFAFGVVLIELLTG+KAMTTKENGEVV+LWWD WKIFD E NEERERLKWMDPKL++YP	531
Sbjct	418	VFAFGVVLIELLTGKAMTTKENGEVVLWWDKFWKIFDLEGNRERERLKWMDPKLESFYP	477
Query	532	IDYALSLAS 540	
Sbjct	478	ID ALSLAS	486

>dbj|BAI79275.1| LysM type receptor kinase [Lotus japonicus]
dbj|BAI79285.1| LysM type receptor kinase [Lotus japonicus]

Length=591

GENE ID: 100380877 LYS11 | LysM type receptor kinase [Lotus japonicus]
(10 or fewer PubMed links)

Score = 706 bits (1823), Expect = 0.0, Method: Compositional matrix adjust.
Identities = 370/606 (61%), Positives = 462/606 (76%), Gaps = 24/606 (3%)

Query	1	MAVFFVSLTLGAQILYVLMFFFTC---IEAQSQQTNTNFSCPSNSPPSCETVTVYISQS M FF+ + + +MF+ I AQ TNGTNFSCP +SPPSC+TVVY +QS	57
Sbjct	1	MTSFFL---FTNTLFLA1MMFFSTTHHILAQLSHTNTNFSCPVDPSCDTVTVYFAQS	57
Query	58	PNFLSLTSVSNIFDTSPSLIARASNLLQHEEDKLIPGQVLLIPVTCGCTGNRSFANISYEI PNFL+LTS+S++FDTSPSLIARASN++ E L+PG+LL+PTC C+G+ SF+NIS+ I	117
Sbjct	58	PNFLTLTSISDLFDTSPSLIARASNIDENQNLVPGQLLVPVTCACSGSNFSNISHMI	117
Query	118	NQGDSFYFVATTLYQNLTNWAVMDLNPGSQFTLPIGIQVVIPLFKCPSKNQLDRGIK +G+S+Y++TT Y+NLTNW V D NP + + LP+G+VVIPLFKCPS L+G+I+	177
Sbjct	118	KEGESYYLSTTSYENLTNWETVQDSNPNNPYLLPGVPGIKVVIPLFKCPSNYHLNKIE	177
Query	178	YLITHWQPNDNNSFVSNKLGASPQDILSENNYQ-QNFTAASNLPVLIPTVLLPDLIQSP YLIT+VW NDNV+ S QDI+SENN+ QNFTAA+P+LPVLT LP L QS	236
Sbjct	178	YLITYVWHNNDNNSVLVASKFGVSTQDIISENNFHSQNFATAATNFP1LIPVTLQPLSLSQSY	237
Query	237	SDGRKHRIGLPLVIIIGISLGCTLLVVVSAIL-LVCVCLMKM--SLNRASSAETA-DKLL S + R II ++ A+L LV V CL+ + S N+S S E A KL+ SSSERKRSNHIHIIISIGISLGLSTLLIALLVLSVTCLRKRKSSENKSLLSVEIAGKKLI	292
Sbjct	238	297	
Query	293	SGVSGYVSKPTMYETGAILEATMNLSEQCKIGESVYKANIEGKVLAVKRFKEDVTEELK SGVS YVSK +YE I+EAT+NL+EQCKIGESVYKA ++G+VLAVK+ KEDVTEEE+ I	352
Sbjct	298	SGVSNYVSKSILYEFRLIMEATLNLNQCKIGESVYKAKLDGQVLAJKVVKEDVTEEVMI	357
Query	353	LQKVNHNGLVKLMLGVSSDNDGNCFVYEAENGSLLEELWFAKSCSETNSRTSLWCRI LQKVNHN GLVKLMLGVSS +DGN F+VYE+AENGSL WLF+ S ++ SR LTW QRI	412
Sbjct	358	LQKVNHNGLVKLMLGVSSGHDGNHFLVYEAENGSLHNWLFSNS--STGSRF-LTWSQRI	413
Query	413	SIAVDVSMGLQYMHEHAYPRIVRHDITSSNILLDSNFKAKIANFSMARTFTNPMMSKIDV SIAVDV+MGLQYMHEH P IVRDITSSNILLDSNFKAKIANFS+ART NPM+ K+DV	472
Sbjct	414	SIAVDVAMGLQYMHEHTQPSIVRHDITSSNILLDSNFKAKIANFSVARTSINPMILKVDV	473
Query	473	FAFGVVLIELLTGRKAMTTKENGEVVMLWWDKIWFIDQEEENREERLKWMDPKLDNYYP F+GVG+ELL+G+K++T N E+ I +IFD +E REER+R+WMDPK++ YPI	532
Sbjct	474	FGYGVVLIELLSGKKSLSLTT--NNEI---NHIREFDLDKEEIRRRWMDPKESLYPI	526
Query	533	DYALSLASLAVNCTADKSLSRPTIAEIVLSSL-TQPSATLERSLTSSGLDVEATQIV D ALSLA LA+NCT++K LSRPT+ E+VLSLSS T Q SP TLERS T GLDV+ T++	591

Subject 527 DDALSLAFLAMNCTSEKPLSRPTMGEVVLSSLMTQHSPTTLERSWT-CGLDVDVTEMQ 585
 Query 592 TSISAR 597
 T I+AR
 Subject 586 TLIAAR 591

>ref|XP_002269472.1| PREDICTED: hypothetical protein [Vitis vinifera]
 emb|CBI17584.3| unnamed protein product [Vitis vinifera]
 Length=590

Gene ID: 100259809 LOC100259809 | hypothetical protein LOC100259809
 [Vitis vinifera] (10 or fewer PubMed links)

Score = 643 bits (1659), Expect = 0.0, Method: Compositional matrix adjust.
 Identities = 329/575 (57%), Positives = 420/575 (73%), Gaps = 6/575 (1%)

Query 25 IEAQSQQTNGTNFSCPSNSPSCPCTVTVYISQSPNFLSLTSVSNIFDTSPLSIARASNLQ 84
 I AQS Q GTNFSC + P C+TYV Y +Q+P FL + ++S+F S LSIA ASN
 Subject 20 ITAQSPATPVTFNSCTTDSPASCQTYVIYRAQAPGFLDVGNISDLFGISRLSIAEASNLA 79

Query 85 HEEDKLIPGQVLLIPVTCGCTGNRSFANISYEINQGDSFYFVATTLYQNLTNWHAVMQL 144
 EE +L P Q+L+P+ C CTGN FANI+Y+I DSFYFV+ T++NLTN+AV LN
 Subject 80 SEEARLSPDQLLVPILCSCTGNHYKIKTDDSFYFVSVTFENLTNYNAVEALN 139

Query 145 PGLSQFTLPIGQVVIPLFCCKCPSKNQLDRGIKYLITHVWQPNDNVSFVSNKLGASPQDI 204
 PGL TL +G+VV PLFCKCPSK+ D+GI YLIT+VWQP D+V V L ASP DI
 Subject 140 PGLEPTTLQVGVEVVFPLFCCKCPSKSHSDKGINYLITYVWQPGDDVLLVGTNLKASPVDI 199

Query 205 LSENNYYGQNFTAASNLPVLIPTVTLPPDLIQSPSDGRKHRIGLPVIIGISLGCTLLVVSA 264
 ENN NF+A+ + PVLIPV+ P L Q K R L +++ S G L+ ++ +
 Subject 200 RDENN-NLNFSASDQPVLIPVSQPPPQTPERRASKGRWLALV--STGALLIFLVS 256

Query 265 ILLVCVCCCLMKMSLNRASSAETAD--KLLSGVSGYVSKPTMYETGAILEATMNLSEQCK 322
 +L+ K K+L S SS ET D KLL GVSGY+ KP MYET I+EATMNL+E +
 Subject 257 LLVYTGLIRKKKTLDHSESSLETTDLIKLPGVSGYLGKPMIYETKVIMEATMNLNEHYR 316

Query 323 IGGSVYKANIEGVLAVERKFKEDVTEELKILQKVNHGNLVKLMGVSSNDGNCFVVVEYAA 382
 IG SVY+A I G+V+AVK+ KE+TEEL+ILQKVNHGNLVKLMGVSSD DGN F+VYE+A
 Subject 317 IGGSVYRATINGQVVAVKKTKEDEITEELRILQKVNHGNLVKLMGVSSDADGNRFLVYFA 376

Query 383 ENGSLEEWLFAKKCSETNSRTSLTWQCQRISIAVDSVSMGLQYMHAYPRIVHRDITSSN 442
 ENGSL+ +WL K S +S+ LTW QRI +A+DV+ GLQYMHAY P +VHDI + +N
 Subject 377 ENGSLDKWLHPKPSSPSSSV-AFLTWSQRIQVALDVANGLQYMHETQPSVVRDIRANN 435

Query 443 ILLDSNFKA KIANFSMARTFTNPMM SKIDVFAFGVVLIELLTGRKAMTTKENGEVVMLWK 502
 ILLDS FKA KIANFSMA N MM K+DVFAGVVL+ELL+G+KAM + NGE+VMLWK
 Subject 436 ILLDSRFKA KIANFSMATT PAMNSMMPKVDFVFAFGVVLLELLSGKQMOMRANGEIVMLWK 495

Query 503 DIWKIFDQEENREERLKWM DP KLDNYY PIDYALSLASLAVN TADKSLSRPTIAEIVLS 562
 DI +I + E+ RE+R+R+WMDP L+N+YP D AL+LA IA +CT +KS +RP+ +AEI +
 Subject 496 DIREILEVEDKREDIRRRWMDP TLLENFPFDGALNLAGLARSTQEKSSARPMAEIAFN 555

Query 563 LSLLTQPSPATLERSLTSSGLDVEATQIVTSISAR 597
 LS+L+Q S TLERS T E QI+ + AR
 Subject 556 LSVLSQTSSETLERSWTQGFPEETIQIINPVIAR 590

>ref|XP_002533280.1| serine-threonine protein kinase, plant-type, putative [Ricinus communis]
 gb|EEF29112.1| serine-threonine protein kinase, plant-type, putative [Ricinus communis]
 Length=620

Gene ID: 8272992 RCOM_0411680 | serine-threonine protein kinase, plant-type, putative [Ricinus communis]

Score = 618 bits (1594), Expect = 6e-175, Method: Compositional matrix adjust.
 Identities = 330/602 (54%), Positives = 420/602 (69%), Gaps = 32/602 (5%)

Query 23 TCIEAQSQQTNGTNFSCPSNSPSCPCTVTVYISQSPNFLSLTSVSNIFDTSPLSIARASN 82
 I AQS Q GTNFSC + P C+TYV Y +Q+P FL + ++S+F S LSIA ASN
 Subject 24 TYVTAQSPQ--GTNFSCSVDLPSPCQTYVAYYAQQPNFLNLGNISDLFAVSRLSIAASN 81

Query 83 LQHEEDKLIPGQVLLIPVTCGCTGNRSFANISYEINQGDSFYFVATTLYQNLTNWHAVM 142
 L E+ L+P Q+L+P+TCGCTGN SFANI+Y+I GDSFYFV+TT ++NL W AV
 Subject 82 LVSEDIPLMNPQLLVPITCGCTGNSSFANITYQIKPGDSFYFVSTTYFENLAKWQAVES 141

Query 143 LNPGLSQFTLPIGQVVIPLFCCKCPSKNQLDRGIKYLITHVWQPNDNVSFVSNKLGASPQ 202
 NP L L G +VV PLFCKCPSKNQ+ GI+YLT+VWQP D++ V K ASP
 Subject 142 FNPNLDPTLLHPGDKVVPLFCCKCPSKNQMKHGIQYLLITYVWQPEDDIFKVGAKFNAPH 201

Query 203 DILSENNYYGQNFTAASNLPVLIPTVTLPPDLIQ-SPSDGRKHRIGLPVIIGISLGCTLLVV 261
 DI +NNY +F+ A+ P+PLFVT +P L Q SPS ++ L +II S+ LL+
 Subject 202 DIAIQNNYW-DFSTAVHHPLLIPVTPQMPLSQSPSPSWPQRSEHHLVIIIVTSVAGALLIF 260

Query 262 VSAILLV---CVVCLMKM--SLNRASSAETA-----DKLLSGVS 296
 + LV C C K K +L+R+ S ET DKLL GVS
 Subject 261 LLVAFLVHAHCSCKKKKTMTHRN GSCLETTDLLQIKEQGKYRSFEPKIIQDKLPGVS 320

Query 297 GYSVKPTMPTGAILEATMNLSEQCKIGESVYKANIEGVLAVERKFKEDVTEELKILQKV 356
 Gy+ KP MY+ IL ATM+L E +IG SVY+A NI G+VLA VK+ K D+TEEL ILQKV
 Subject 321 GYLGKPMIYDIKEILLATMDLHEHYRIGGSVYRANINGQVLA VVKTKVDITEELNILQKV 380

Query 357 NHGNLVKLMGVSSNDGNCFVVVEYEAENGSLLEEWLFAKKCSETNSRTSLTWQCQRISIAV 416
 NH NLV KLMG+SS+ DG+CF+VYEYAENGSL+ +WL K + +S+S L+W QR+ IA+
 Subject 381 NHANLVKLMGISSNADGDFCLVYEYAENGSLDWKLHPKP-ASSSSSVAFLWSQRLQIAL 439

Query 417 DVSMGLQYMHAYPRIVHRDITSSNILLDSNFKA KIANFSMARTFTNPMM SKIDVFAFG 476
 DV+ GLQYMHAY P +VH DI +SNILDS FKA KIANFS+A+ T+ M+ K+DVFAGF
 Subject 440 DVASGLQYMHHEHQPTVVHMDIRTSNILLDSRFKA KIANFSVAKLTTDSMLQKVDFVFAFG 499

Query 477 VVLLIELLTGRKAMTTKENGEVVMWLWDK1WKFIDQDEENREERLKWM DP KLDNYY PIDYAL 536
 VVLLIELL G+KAM T ENGE+V+LWK++ + + E R ERL+K MDP L+N+YPID AL
 Subject 500 VVLLLELCGKKA MVTNENGEIVLLWKE MVAEKRAERLKRM DP LENFYPIDSAL 559

Query 537 SLASLAVNCTADKSLRPTIAEIVLSSLTQPSATLERSLTSSGLDVEA-TQIVTSIS 595
 SLA+LA CT +KS +RP++AEIV +L++LTQ TLERS T SGL+ E QI + +
 Sbjct 560 SLANLARVCTLEKSSARPSMAEIVFNLTVLTQSCSETLERSWT-SGLEAEEDIQITSPVI 618
 AR 597
 AR 620

>**ref|XP_002310198.1|** predicted protein [Populus trichocarpa]
gb|EEE90648.1| predicted protein [Populus trichocarpa]
 Length=601
Gene ID: 7473142 POPTRDRAFT_870366 | hypothetical protein [Populus trichocarpa]
 (10 or fewer PubMed links)

Score = 595 bits (1534), Expect = 7e-168, Method: Compositional matrix adjust.
 Identities = 321/607 (52%), Positives = 425/607 (70%), Gaps = 16/607 (2%)

Query 1 MAVFFVSLTLGAQILYVVLMMFTCIEAQSQQTNGTNFSCPSNSPPSCETYVTYISQSPNF 60
 MA+ +S + +V+ +F+ +Q GTNFSCP +SP SC TY++Y+Q P+F
 Sbjct 1 MAISLLSSFFTQALFFLVLVFFSTY-VTAQAPPGTNFSCPVDSPCTSYLAQPPDF 59
 Query 61 LSLTSVSNIFDTSPSLSIARASNLIQHEEDKLIPGQVLLIPVTCCTGNRSFANISYEINQ 120
 L +S++F S IA ASNLI E+ L P Q+LL+P+ CGCTG++SF NI+Y+I QG
 Sbjct 60 LDLGKISHLFGISRTLIASASNIVNSEDTPLFPNQLLIVPIRCCTGSQSFSVNITYQIQQQG 119
 Query 121 DSFYFVATTLYQNLTNWHAVMDLNPGLSQFTLPIGIQVVIPLFCKCPSKNQLDRGIKYLI 180
 DS Y V+T +NLNT W V LN L+ L G +V+ PLFKCKPS+ L+ GI++LI
 Sbjct 120 DSIYSVSTISFENLTRWQEVEALNRSILTPTLLHAGDEVIFPLFKCPSPRTHLENGIEHLI 179
 Query 181 THVWQPNDNVSVFSNKNLKGASPQDILSENNYGQNFTAASNLNPVLIPTVTPDLIQQ--SPS 237
 T+VWQP D++ V+ L AS ++I+ ENNY NF AA P+IPV+ LP L Q +P
 Sbjct 180 TYVWQPQGDDLKVKVAAMLNASENRIVIENNY-DNFNAAVYNPIVPSKLPVLSQPYLTPE 238
 Query 238 D-GRKHRIGLPVIIGISLGCTLLVV-VSAILLVCVCLK-MKSLSNRASSAETAD--KLL 292
 G KH VI+ S+ T + A L+ C K K+L+R+ S ET+D KLL
 Sbjct 239 RRGSKHL--WIVIVAASTASTFTTCPLVAFLIHKRCSYKATKALDRTGSCLETSDPKLL 296
 Query 293 SGVSGYVSKPTMLETGAIILEATMNLSEQCKIGESVYKANIEGVLAJKRFKEVTEELKI 352
 GV G + K +YE AI+E TM+L E KIG SVY+ANI G VLAVK+ K+DVTEELKI
 Sbjct 297 PGVLGCLDKSIIYEVKAIMEGTMMDLHEHYKIGGSVYRANINGCVLAVRKTKDVTTEELKI 356
 Query 353 LQKVNHGNLVLKLMGVSSDND--GCNFVVYEEYAENGSLLEWLFAKSCSETNSRSTS LTWCQ 410
 LQKV+H NLVKLMG+SS++D GN F+VVEYAENGSL+WL KS +S+S LTW Q
 Sbjct 357 LQKVSHANLVLKLMGMSSESREGNRFLVYEEYAENGSLDKWLHPKS-ESSSSSVGFLTWKQ 415
 Query 411 RISIAVDVSMGLQYMHEAYPPIRHRDITSSNILLDSNFKAKIANFSMARTFTNPMMMSKI 470
 R+ +A+D+V+ GLQY+HEH PR VH+DI +SNILDS F+AKIANFSMAR T+ MM K
 Sbjct 416 RMQVALDVANGLQYLHEHTQPRVHKDIRTSNILLSTFRAKIANFSMARAATDSMPKD 475
 Query 471 DVFAFGVVLIELLTGRKAMTTKENGEVVMLWLDIWKIFDQEENREERLRKWMKPDKLDNYY 530
 DVF FGVVL+ELL+G+KAM TKE GE+V+L ++I + + EE REERLRKWMKPDKL+ +Y
 Sbjct 476 DVDFGVVLLLENGKVKAMTKEKGEIVLLCREIKDVLEEMEEKRERLRKWMDPNLERFY 535
 Query 531 PIDYALSLASLAVNCTADKSLRPTIAEIVLSSLTQPSATLERSLTSSGLDVEATQI 590
 PID A+SLA+LA CT +KS RP++AEIV +L++LTQ SP TLER TS + T++
 Sbjct 536 PIDSAMSLATLARLCTLEKSSERPSMAEIVFNLTVLTQSSPETLER-WTSEVETEDFTRL 594
 Query 591 VTSSISAR 597
 V+ ++AR
 Sbjct 595 VSPVTAR 601

>**gb|ADJ19109.1|** truncated Nod-factor receptor 5A [Glycine max]
 Length=337

Gene ID: 100498858 NFR5a | Nod-factor receptor 5A [Glycine max]
 (10 or fewer PubMed links)

Score = 536 bits (1381), Expect = 4e-150, Method: Compositional matrix adjust.
 Identities = 277/337 (82%), Positives = 301/337 (89%), Gaps = 1/337 (0%)

Query 1 MAVFFVSLTLGAQILYVVLMMFTCIEAQSQQTNGTNFSCPSNSPPSCETYVTYISQSPN 59
 MAVFF L L +QIL +V+M F T I AQSQQ N TNFSCPS+SPPSCETYVTYI+QSPN
 Sbjct 1 MAVFFPFLPLHSQILCLVIMLFSTNIVAQSQQDNRNTNFSCPSDPPSCETYVTYIAQSPN 60
 Query 60 FLSLTSVSNIFDTSPSLSIARASNLIQHEEDKLIPGQVLLIPVTCCTGNRSFANISYEINQ 119
 FLSLT+ +SNIFDTSPSLSTARASNLIQHEEDKLIPGQVLLIPVTCCTGNRSFANISYEINQ
 Sbjct 61 FLSLTNISNIFDTSPSLSTARASNLEPMDDKLVRDQVLLIPVTCCTGNRSFANISYEINQ 120
 Query 120 GDSFYFVATTLYQNLTNWHAVMDLNPGLSQFTLPIGIQVVIPLFCKCP SKNQLDRGIKYL 179
 GDSFYFVATT Y+NLTNW AVMDLN PLS LPIGIQVVIPLFCKCP SKNQLD+ IKYL
 Sbjct 121 GDSFYFVATT SYENL TNWRAVM DLPVLS PNLPIG I QVVFPLFCKCP SKNQLDKEIKYL 180
 Query 180 ITBVWQPNDNVSVFSNKNLKGASPQDILSENNYGQNFTAASNLNPVLIPTVTPDLIQQPSDG 239
 IT+VW+P DNVS VS+K GASP+DI+SENNYGQNFTAASNLNPVLIPTVTPDLIQQPSDG
 Sbjct 181 ITYVWKPQGDNVSLVSDKFVGASPEDIMSENNYGQNFTAANNLPVLIPTVTPDLVPLARSPDG 240
 Query 240 RKHRIGLPVIIGISLGCTLLVVSAILLVCVCLKMKS LNRASSAETADKLLSGVSGYV 299
 RK I LPVIIGISLGCTLLVV A+LLV V CLKMK+LNRASSAETADKLLSGVSGYV
 Sbjct 241 RKGGIRLPVIIGISLGCTLLVVLA VLLVYVYCLKMKT LNRASSAETADKLLSGVSGYV 300
 Query 300 SKPTMYETGAIILEATMNLSEQCKIGESVYKANIEGV 336
 SKPTMYET AI+EATMNLSEQCKIGESVYKANIEGV
 Sbjct 301 SKPTMYETDAIMEATMNLSEQCKIGESVYKANIEGV 337

>**dbj|BAG85147.1|** Nod factor receptor protein [Glycine soja]
 Length=327

Score = 519 bits (1337), Expect = 4e-145, Method: Compositional matrix adjust.
 Identities = 261/327 (79%), Positives = 285/327 (87%), Gaps = 1/327 (0%)

Query 5 FVSLTLGAQILYVVLMMFTCIEAQSQQTNGTNFSCPSNSPPSCETYVTYISQSPNFLSL 63
 F L L +QIL +V+M F T I AQSQQ N TNFSCPS+SPPSCETYVTYI+QSPNFLSL

Subject 1 FFLPLHSQILCIVIMLFSTNIVAQSQDNRTNFSCPSDPPSCETYVTYIAQSPNFLSL 60
 Query 64 TSVSNIFDTSPSIIARASNLQHEEDKLI PGQVLLIPVTCGCTGNRSFANISYEINQGDSF 123
 T++SNIFDTSPSIIARASNL+ +DKL+ QVLL+PVTCGCTGNRSFAN SYEINQGDSF
 Subject 61 TNISNIFDTSPSIIARASNLPEMDDKLVKDQVLLVPVTCGCTGNRSFANTSYEINQGDSF 120
 Query 124 YFWATTLYQNLTNWHAVMDDLNPGLSQFTLPIGIQVVIPLFCCKPSKNQLDRGIKYLITHV 183
 YFWATT Y+NLTNW AVMDLNP LS LPIGIQVV PLFCKCPSKNQLD+ IKYLIT+V
 Subject 121 YFWATTSYENLTNWRAVMDDLNPLVSPNKLPIGIQVVFPLFCCKPSKNQLDKEIKYLITYV 180
 Query 184 WQPNDNVSFSVSNKLGAQDILSENNYQGNFTAASNLPVLPVTLPLIQSPPSDGRKHR 243
 W+P DNVS VS+K GASP+DI+SSENNYQGNFTAANLPVLPVTLPLIQSPPSDGRKHR
 Subject 181 WKPGDNVSLVSDKFGASPEDIMSENNYQGNFTAANNLPVLPVTRLPVLARSPSDGRKGG 240
 Query 244 IGLPVIIGISLGCTLLVVVSAILLCVCCMKMSLNRSASSAETADKLLSGVSGYVSKPT 303
 I LPVIIGI+LGCTLLV+A CLKMK+LNRASSAETADKLLSGVSGYVSKPT
 Subject 241 IRLPVIIGISLGCTLLVLAFLVLYVYCLKMKTLNRSASSAETADKLLSGVSGYVSKPT 300
 Query 304 MYETGAIIEATMNLSEQCKIGESVYKA 330
 MYET AI+EATMNLSEQCKIGESVYKA
 Subject 301 MYETDAIMEATMNLSEQCKIGESVYKA 327

>dbj|BAG85143.1| Nod factor receptor protein [Glycine soja]
 dbj|BAG85149.1| Nod factor receptor protein [Glycine soja]
 dbj|BAG85156.1| Nod factor receptor protein [Glycine soja]
 11 more sequence titles

dbj|BAG85159.1| Nod factor receptor protein [Glycine max]
 dbj|BAG85160.1| Nod factor receptor protein [Glycine max]
 dbj|BAG85161.1| Nod factor receptor protein [Glycine max]
 dbj|BAG85162.1| Nod factor receptor protein [Glycine max]
 dbj|BAG85165.1| Nod factor receptor protein [Glycine max]
 dbj|BAG85168.1| Nod factor receptor protein [Glycine max]
 dbj|BAG85171.1| Nod factor receptor protein [Glycine max]
 dbj|BAG85174.1| Nod factor receptor protein [Glycine max]
 dbj|BAG85177.1| Nod factor receptor protein [Glycine max]
 dbj|BAG85179.1| Nod factor receptor protein [Glycine max]
 dbj|BAG85180.1| Nod factor receptor protein [Glycine max]

Length=327

Score = 516 bits (1329), Expect = 3e-144, Method: Compositional matrix adjust.
 Identities = 267/327 (81%), Positives = 291/327 (88%), Gaps = 1/327 (0%)

Query 5 FVSLTLGAQILYVVLMMFF-TCIEAQSQQTNGTNFSCPSNSPPSCETYVTYIQSPPNFLSL 63
 F L L +QIL +V+M F T I AQSQQ N TNFSCPS+SPPSCETYVTYI+QSPPNFLSL
 Subject 1 FFLPLHSQILCIVIMLFSTNIVAQSQDNRTNFSCPSDPPSCETYVTYIAQSPNFLSL 60
 Query 64 TSVSNIFDTSPSIIARASNLQHEEDKLI PGQVLLIPVTCGCTGNRSFANISYEINQGDSF 123
 T++SNIFDTSPSIIARASNL+ +DKL+ QVLL+PVTCGCTGNRSFANISYEINQGDSF
 Subject 61 TNISNIFDTSPSIIARASNLPEMDDKLVKDQVLLVPVTCGCTGNRSFANISYEINQGDSF 120
 Query 124 YFWATTLYQNLTNWHAVMDDLNPGLSQFTLPIGIQVVIPLFCCKPSKNQLDRGIKYLITHV 183
 YFWATT Y+NLTNW AVMDLNP LS LPIGIQVV PLFCKCPSKNQLD+ IKYLIT+V
 Subject 121 YFWATTSYENLTNWRAVMDDLNPLVSPNKLPIGIQVVFPLFCCKPSKNQLDKEIKYLITYV 180
 Query 184 WQPNDNVSFSVSNKLGAQDILSENNYQGNFTAASNLPVLPVTLPLIQSPPSDGRKHR 243
 W+P DNVS VS+K GASP+DI+SSENNYQGNFTAANLPVLPVTLPLIQSPPSDGRKHR
 Subject 181 WKPGDNVSLVSDKFGASPEDIMSENNYQGNFTAANNLPVLPVTRLPVLARSPSDGRKGG 240
 Query 244 IGLPVIIGISLGCTLLVVVSAILLCVCCMKMSLNRSASSAETADKLLSGVSGYVSKPT 303
 I LPVIIGI+LGCTLLV+A+LL V CLKMK+LNRASSAETADKLLSGVSGYVSKPT
 Subject 241 IRLPVIIGISLGCTLLVLAFLVLYVYCLKMKTLNRSASSAETADKLLSGVSGYVSKPT 300
 Query 304 MYETGAIIEATMNLSEQCKIGESVYKA 330
 MYET AI+EATMNLSEQCKIGESVYKA
 Subject 301 MYETDAIMEATMNLSEQCKIGESVYKA 327

>dbj|BAG85152.1| Nod factor receptor protein [Glycine soja]
 Length=327

Score = 516 bits (1328), Expect = 5e-144, Method: Compositional matrix adjust.
 Identities = 267/327 (81%), Positives = 290/327 (88%), Gaps = 1/327 (0%)

Query 5 FVSLTLGAQILYVVLMMFF-TCIEAQSQQTNGTNFSCPSNSPPSCETYVTYIQSPPNFLSL 63
 F L L +QIL +V+M F T I AQSQQ N TNFSCPS+SPPSCETYVTYI+QSPPNFLSL
 Subject 1 FFLPLHSQILCIVIMLFSTNIVAQSQDNRTNFSCPSDPPSCETYVTYIAQSPNFLSL 60
 Query 64 TSVSNIFDTSPSIIARASNLQHEEDKLI PGQVLLIPVTCGCTGNRSFANISYEINQGDSF 123
 T++SNIFDTSPSIIARASNL+ +DKL+ QVLL+PVTCGCTGNRSFANISYEINQGDSF
 Subject 61 TNISNIFDTSPSIIARASNLPEMDDKLVKDQVLLVPVTCGCTGNRSFANISYEINQGDSF 120
 Query 124 YFWATTLYQNLTNWHAVMDDLNPGLSQFTLPIGIQVVIPLFCCKPSKNQLDRGIKYLITHV 183
 YFWATT Y+NLTNW AVMDLNP LS LPIGIQVV PLFCKCPSKNQLD+ IKYLIT+V
 Subject 121 YFWATTSYENLTNWRAVMDDLNPLVSPNKLPIGIQVVFPLFCCKPSKNQLDKEIKYLITYV 180
 Query 184 WQPNDNVSFSVSNKLGAQDILSENNYQGNFTAASNLPVLPVTLPLIQSPPSDGRKHR 243
 W+P DNVS VS+K GASP+DI+SSENNYQGNFTAANLPVLPVTLPLIQSPPSDGRKHR
 Subject 181 WKPGDNVSLVSDKFGASPEDIMSENNYQGNFTAANNLPVLPVTRLPVLARSPSDGRKGG 240
 Query 244 IGLPVIIGISLGCTLLVVVSAILLCVCCMKMSLNRSASSAETADKLLSGVSGYVSKPT 303
 I LPVIIGI+LGCTLLV+A+LL V CLKMK+LNRASSAETADKLLSGVSGYVSKPT
 Subject 241 IRLPVIIGISLGCTLLVLAFLVLYVYCLKMKTLNRSASSAETADKLLSGVSGYVSKPT 300
 Query 304 MYETGAIIEATMNLSEQCKIGESVYKA 330
 MYET AI+EATMNLSEQCKIGESVYKA
 Subject 301 MYETDAIMEATMNLSEQCKIGESVYKA 327

>dbj|BAG85148.1| Nod factor receptor protein [Glycine soja]
 Length=327

Score = 515 bits (1327), Expect = 5e-144, Method: Compositional matrix adjust.
 Identities = 266/327 (81%), Positives = 291/327 (88%), Gaps = 1/327 (0%)

Query 5 FVSLTLGAQILYVVLMMFF-TCIEAQSQQTNGTNFSCPSNSPPSCETYVTYIQSPPNFLSL 63

Sbjct 1 F L L +QIL +V+M F T I AQSQQ N TNFSCPS+SPPSCETYVTYI+QSPNFLSL
 FPFLPLHSQILC1VLIMLFSTNIVAQSQSQDNRTNFSCPSDPPSCETYVTYIAQSPNFLSL 60

Query 64 TSVSNIFDTSPLSIARASNLQHEEDKLI PGQVLLIPVTCGCTGNRSFANISYEINQGDSF 123
 T++SNIFDTSPLS+ARASNL+ +DKL+ QVLL+PVTGCGCTGNRSFANISYEINQGDSF
 Sbjct 61 TNISNIFDTSPLSVARASNLEPMDDKLKVQDQVLLPVTCGCTGNRSFANISYEINQGDSF 120

Query 124 YFVATTLYQNLTNWHAVMMDLNPGLSQFTLPIGIQVVIPLFCKCPSKNQLDRGIKYLITHV 183
 YFVATT Y+NLTNW AVMDLNP LS LPIGIQVV PLFCKCPSKNQLD+ IKYLIT+V
 Sbjct 121 YFVATTTSYENLTNWRAVMDLNPVLPNKLPIGIQVVFPLFCKCPSKNQLDKEIKYLITYV 180

Query 184 WQPNNDNSFVSNSNKGASPQDILSENNYQNFNTAASNLPLVLPVTLPLDIQSPSDGRKHR 243
 W+P DNVS VS+K GASP+DI+SENNYQNFNTAA+NLPVLPVPT LP L +SPSDGRK
 Sbjct 181 WKPGDNVSLVSDKFGASPEDIMSENNYQNFNTAANNLPLVLPVTRLPVLARSPSDGRKGG 240

Query 244 IGLPVIIGISLGCTLLVVSAI1LVCVCLMKMSLNRSASSAETADKLLSGVGSGYVSKPT 303
 I LPVIIGISLGCTLLV+V A+LLV V CLKMK+LNRSSAETADKLLSGVGSGYVSKPT
 Sbjct 241 IRLPVIIGISLGCTLLVLVLAVALVYVYCLKMKTLNRSASSAETADKLLSGVGSGYVSKPT 300

Query 304 MYETGAILEATMNLSSEQCKIGESVYKA 330
 MYET AI+EATMNLSSEQCKIGESVYKA
 Sbjct 301 MYETDAIMEATMNLSSEQCKIGESVYKA 327

>**dbj|BAG85178.1|** Nod factor receptor protein [Glycine max]
 Length=327

Gene ID: 100498858 NFR5a | Nod-factor receptor 5A [Glycine max]
 (10 or fewer PubMed links)

Score = 514 bits (1325), Expect = 9e-144, Method: Compositional matrix adjust.
 Identities = 266/327 (81%), Positives = 291/327 (88%), Gaps = 1/327 (0%)

Query 5 FVSLTLGAQILYVVLMMFF-TCIEAQSQQTNGTNFSCPSNSPPSCETYVTYI+QSPNFLSL 63
 F L L +QIL +V+M F T I AQSQQ N TNFSCPS+SPPSCETYVTYI+QSPNFLSL
 Sbjct 1 FPFLPLHSQILC1VLIMLFSTNIVAQSQSQDNRTNFSCPSDPPSCETYVTYIAQSPNFLSL 60

Query 64 TSVSNIFDTSPLSIARASNLQHEEDKLI PGQVLLIPVTCGCTGNRSFANISYEINQGDSF 123
 T++SNIFDT+PLSIARASNL+ +DKL+ QVLL+PVTGCGCTGNRSFANISYEINQGDSF
 Sbjct 61 TNISNIFDTSPLSIARASNLQHEEDKLI PGQVLLIPVTCGCTGNRSFANISYEINQGDSF 120

Query 124 YFVATTLYQNLTNWHAVMMDLNPGLSQFTLPIGIQVVIPLFCKCPSKNQLDRGIKYLITHV 183
 YFVATT Y+NLTNW AVMDLNP LS LPIGIQVV PLFCKCPSKNQLD+ IKYLIT+V
 Sbjct 121 YFVATTTSYENLTNWRAVMDLNPVLPNKLPIGIQVVFPLFCKCPSKNQLDKEIKYLITYV 180

Query 184 WQPNNDNSFVSNSNKGASPQDILSENNYQNFNTAASNLPLVLPVTLPLDIQSPSDGRKHR 243
 W+P DNVS VS+K GASP+DI+SENNYQNFNTAA+NLPVLPVPT LP L +SPSDGRK
 Sbjct 181 WKPGDNVSLVSDKFGASPEDIMSENNYQNFNTAANNLPLVLPVTRLPVLARSPSDGRKGG 240

Query 244 IGLPVIIGISLGCTLLVVSAI1LVCVCLMKMSLNRSASSAETADKLLSGVGSGYVSKPT 303
 I LPVIIGISLGCTLLV+V A+LLV V CLKMK+LNRSSAETADKLLSGVGSGYVSKPT
 Sbjct 241 IRLPVIIGISLGCTLLVLVLAVALVYVYCLKMKTLNRSASSAETADKLLSGVGSGYVSKPT 300

Query 304 MYETGAILEATMNLSSEQCKIGESVYKA 330
 MYET AI+EATMNLSSEQCKIGESVYKA
 Sbjct 301 MYETDAIMEATMNLSSEQCKIGESVYKA 327

>**dbj|BAG85144.1|** Nod factor receptor protein [Glycine soja]
dbj|BAG85145.1| Nod factor receptor protein [Glycine soja]
 Length=327

Score = 514 bits (1325), Expect = 1e-143, Method: Compositional matrix adjust.
 Identities = 267/327 (81%), Positives = 290/327 (88%), Gaps = 1/327 (0%)

Query 5 FVSLTLGAQILYVVLMMFF-TCIEAQSQQTNGTNFSCPSNSPPSCETYVTYI+QSPNFLSL 63
 F L L +QIL +V+M F T I AQSQQ N TNFSCPS+SPPSCETYVTYI+QSPNFLSL
 Sbjct 1 FPFLPLHFQILC1VLIMLFSTNIVAQSQSQDNRTNFSCPSDPPSCETYVTYIAQSPNFLSL 60

Query 64 TSVSNIFDTSPLSIARASNLQHEEDKLI PGQVLLIPVTCGCTGNRSFANISYEINQGDSF 123
 T++SNIFDT+PLSIARASNL+ +DKL+ QVLL+PVTGCGCTGNRSFANISYEINQGDSF
 Sbjct 61 TNISNIFDTSPLSIARASNLQHEEDKLI PGQVLLIPVTCGCTGNRSFANISYEINQGDSF 120

Query 124 YFVATTLYQNLTNWHAVMMDLNPGLSQFTLPIGIQVVIPLFCKCPSKNQLDRGIKYLITHV 183
 YFVATT Y+NLTNW AVMDLNP LS LPIGIQVV PLFCKCPSKNQLD+ IKYLIT+V
 Sbjct 121 YFVATTTSYENLTNWRAVMDLNPVLPNKLPIGIQVVFPLFCKCPSKNQLDKEIKYLITYV 180

Query 184 WQPNNDNSFVSNSNKGASPQDILSENNYQNFNTAASNLPLVLPVTLPLDIQSPSDGRKHR 243
 W+P DNVS VS+K GASP+DI+SENNYQNFNTAA+NLPVLPVPT LP L +SPSDGRK
 Sbjct 181 WKPGDNVSLVSDKFGASPEDIMSENNYQNFNTAANNLPLVLPVTRLPVLARSPSDGRKGG 240

Query 244 IGLPVIIGISLGCTLLVVSAI1LVCVCLMKMSLNRSASSAETADKLLSGVGSGYVSKPT 303
 I LPVIIGISLGCTLLV+V A+LLV V CLKMK+LNRSSAETADKLLSGVGSGYVSKPT
 Sbjct 241 IRLPVIIGISLGCTLLVLVLAVALVYVYCLKMKTLNRSASSAETADKLLSGVGSGYVSKPT 300

Query 304 MYETGAILEATMNLSSEQCKIGESVYKA 330
 MYET AI+EATMNLSSEQCKIGESVYKA
 Sbjct 301 MYETDAIMEATMNLSSEQCKIGESVYKA 327

>**dbj|BAG85170.1|** Nod factor receptor protein [Glycine max]
 Length=327

Score = 514 bits (1325), Expect = 1e-143, Method: Compositional matrix adjust.
 Identities = 266/327 (81%), Positives = 291/327 (88%), Gaps = 1/327 (0%)

Query 5 FVSLTLGAQILYVVLMMFF-TCIEAQSQQTNGTNFSCPSNSPPSCETYVTYI+QSPNFLSL 63
 F L L +QIL +V+M F T I AQSQQ N TNFSCPS+SPPSCETYVTYI+QSPNFLSL
 Sbjct 1 FPFLPLHSQILC1VLIMLFSTNIVAQSQSQDNRTNFSCPSDPPSCETYVTYIAQSPNFLSL 60

Query 64 TSVSNIFDTSPLSIARASNLQHEEDKLI PGQVLLIPVTCGCTGNRSFANISYEINQGDSF 123
 T++SNIFDT+PLSIARASNL+ +DKL+ QVLL+PVTGCGCTGNRSFA+ISEINQGDSF
 Sbjct 61 TNISNIFDTSPLSIARASNLQHEEDKLI PGQVLLIPVTCGCTGNRSFA+ISEINQGDSF 120

Query 124 YFVATTLYQNLTNWHAVMMDLNPGLSQFTLPIGIQVVIPLFCKCPSKNQLDRGIKYLITHV 183
 YFVATT Y+NLTNW AVMDLNP LS LPIGIQVV PLFCKCPSKNQLD+ IKYLIT+V
 Sbjct 121 YFVATTTSYENLTNWRAVMDLNPVLPNKLPIGIQVVFPLFCKCPSKNQLDKEIKYLITYV 180

Query 184 WQPNDNVSFVSNKLGASPQDILSENNYQNFATAASNLPVLPVTLLPDLIQSPSDGRKHR 243
 W+P DNVS VS+K GASP+DI+SENNYQNFATAA+NLPVLIPVT LP L +SPSDGRK
 Sbjct 181 WKPGDNVSLVSDKFGASPEDIMSENNYQNFATAANLPLVLPVRLPVLARSPSDGRKGG 240

Query 244 IGLPVIIGISLGCCTLLVVVSAILLVCVCLMKMSLNRSASSAETADKLLSGVSGYVSKPT 303
 I LPVIIGISLGCCTLLV+A+LLV V CLKMK+LNRSSAAETADKLLSGVSGYVSKPT
 Sbjct 241 IRLPVIIGISLGCCTLLVLVLAVALLVYVYCLKMKTNRSSAAETADKLLSGVSGYVSKPT 300

Query 304 MYETGAILEATMNLSEQCKIGESVYKA 330
 MYET AI+EATMNLSEQCKIGESVYKA
 Sbjct 301 MYETDAIMEATMNLSEQCKIGESVYKA 327

>**dbj|BAG85167.1| Nod factor receptor protein [Glycine max]**
 Length=327

Score = 514 bits (1325), Expect = 1e-143, Method: Compositional matrix adjust.
 Identities = 266/327 (81%), Positives = 290/327 (88%), Gaps = 1/327 (0%)

Query 5 FVSLTLGAQI LYVVLMLFF-TCIEAQSQQTNGTNFSCPSNSPPSCETYVTVI+QSPNFLSL 63
 F L L +QIL +V+M F T I AQSQQ N TNFSCPS+SPPSCETYVTVI+QSPNFLSL 60
 Sbjct 1 FPFLPLHSQI LCLVIMLFSTNIVQAQSQQDNRTNFSCPSDSPPSCETYVTVI+QSPNFLSL

Query 64 TSVSNIFDTSPSLSIARASNLQHEEDKLI PGQVILLIPVTCGCTGNRSFANISYEINQGDSF 123
 ++SNIFDTSPSLSIARASNL+ +DKL+ QVLL+PVTCGCTGNRSFANISYEINQGDSF
 Sbjct 61 ANISNIFDTSPSLSIARASNL EPMDDKLKVQDQVLLPVTCGCTGNRSFANISYEINQGDSF 120

Query 124 YFVATTLYQNLNTNWHAVMDLNPGLSQFTLPIGIVQVVIPLFCCKCP SKNQLDRGIKYLITHV 183
 YFVATT Y+NLNTW AVMDLNP LS LPIGIVQVV PLFCKCP SKNQLD+ IKYLIT+V
 Sbjct 121 YFVATTTSYENLTNWRAVMMDLNPVLPSPNKLPIGIVQVVFPLFCCKCP SKNQLDKEIKYLITYV 180

Query 184 WQPNDNVSFVSNKLGASPQDILSENNYQNFATAASNLPVLPVTLLPDLIQSPSDGRKHR 243
 W+P DNVS VS+K GASP+DI+SENNYQNFATAA+NLPVLIPVT LP L +SPSDGRK
 Sbjct 181 WKPGDNVSLVSDKFGASPEDIMSENNYQNFATAANLPLVLPVRLPVLARSPSDGRKGG 240

Query 244 IGLPVIIGISLGCCTLLVVVSAILLVCVCLMKMSLNRSASSAETADKLLSGVSGYVSKPT 303
 I LPVIIGISLGCCTLLV+A+LLV V CLKMK+LNRSSAAETADKLLSGVSGYVSKPT
 Sbjct 241 IRLPVIIGISLGCCTLLVLVLAVALLVYVYCLKMKTNRSSAAETADKLLSGVSGYVSKPT 300

Query 304 MYETGAILEATMNLSEQCKIGESVYKA 330
 MYET AI+EATMNLSEQCKIGESVYKA
 Sbjct 301 MYETDAIMEATMNLSEQCKIGESVYKA 327

>**dbj|BAG85164.1| Nod factor receptor protein [Glycine max]**
 Length=327

Score = 514 bits (1325), Expect = 1e-143, Method: Compositional matrix adjust.
 Identities = 266/327 (81%), Positives = 290/327 (88%), Gaps = 1/327 (0%)

Query 5 FVSLTLGAQI LYVVLMLFF-TCIEAQSQQTNGTNFSCPSNSPPSCETYVTVI+QSPNFLSL 63
 F L L +QIL +V+M F T I AQSQQ N TNFSCPS+SPPSCETYVTVI+QSPNFLSL 60
 Sbjct 1 FPFLPLHSQI LCLVIMLFSTNIVQAQSQQDNRTNFSCPSDSPPSCETYVTVI+QSPNFLSL

Query 64 TSVSNIFDTSPSLSIARASNLQHEEDKLI PGQVILLIPVTCGCTGNRSFANISYEINQGDSF 123
 ++SNIFDTSPSLSIARASNL+ +DKL+ QVLL+PVTCGCTGNRSFANISYEINQGDSF
 Sbjct 61 TNISNIFDTSPSLSIARASNL EPMDDKLKVQDQVLLPVTCGCTGNRSFANISYEINQGDSF 120

Query 124 YFVATTLYQNLNTNWHAVMDLNPGLSQFTLPIGIVQVVIPLFCCKCP SKNQLDRGIKYLITHV 183
 YFVATT Y+NLNTW AVMDLNP LS LPIGIVQVV PLFCKCP SKNQLD+ IKYLIT+V
 Sbjct 121 YFVATTTSYENLTNWRAVMMDLNPVLPSPNKLPIGIVQVVFPLFCCKCP SKNQLDKEIKYLITYV 180

Query 184 WQPNDNVSFVSNKLGASPQDILSENNYQNFATAASNLPVLPVTLLPDLIQSPSDGRKHR 243
 W+P DNVS VS+K GASP+DI+SENNYQNFATAA+NLPVLIPVT LP L +SPSDGRK
 Sbjct 181 WKPGDNVSLVSDKFGASPEDIMSENNYQNFATAANLPLVLPVRLPVLARSPSDGRKGG 240

Query 244 IGLPVIIGISLGCCTLLVVVSAILLVCVCLMKMSLNRSASSAETADKLLSGVSGYVSKPT 303
 I LPVIIGISLGCCTLLV+A+LLV V CLKMK+LNRSSAAETADKLLSGVSGYVSKPT
 Sbjct 241 IRLPVIIGISLGCCTLLVLVLAVALLVYVYCLKMKTNRSSAAETADKLLSGVSGYVSKPT 300

Query 304 MYETGAILEATMNLSEQCKIGESVYKA 330
 MYET AI+EATMNLSEQCKIGESVYKA
 Sbjct 301 MYEADAIMEATMNLSEQCKIGESVYKA 327

>**dbj|BAG85151.1| Nod factor receptor protein [Glycine soja]**
 Length=327

Score = 514 bits (1324), Expect = 1e-143, Method: Compositional matrix adjust.
 Identities = 266/327 (81%), Positives = 291/327 (88%), Gaps = 1/327 (0%)

Query 5 FVSLTLGAQI LYVVLMLFF-TCIEAQSQQTNGTNFSCPSNSPPSCETYVTVI+QSPNFLSL 63
 F L L +QIL +V+M F T I AQSQQ N TNFSCPS+SPPSCETYVTVI+QSPNFLSL 60
 Sbjct 1 FPFLPLHSQI LCLVIMLFSTNIVQAQSQQDNRTNFSCPSDSPPSCETYVTVI+QSPNFLSL

Query 64 TSVSNIFDTSPSLSIARASNLQHEEDKLI PGQVILLIPVTCGCTGNRSFANISYEINQGDSF 123
 ++SNIFDTSPSLSIARASNL+ +DKL+ QVLL+PVTCGCTGNRSFANISYEINQGDSF
 Sbjct 61 TNISNIFDTSPSLSIARASNL EPMDDKLKVQDQVLLPVTCGCTGNRSFANISYEINQGDSF 120

Query 124 YFVATTLYQNLNTNWHAVMDLNPGLSQFTLPIGIVQVVIPLFCCKCP SKNQLDRGIKYLITHV 183
 YFVATT Y+NLNTW AVMDLNP LS LPIGIVQVV PLFCKCP SKNQLD+ IKYLIT+V
 Sbjct 121 YFVATTTSYENLTNWRAVMMDLNPVLPSPNKLPIGIVQVVFPLFCCKCP SKNQLDKEIKYLITYV 180

Query 184 WQPNDNVSFVSNKLGASPQDILSENNYQNFATAASNLPVLPVTLLPDLIQSPSDGRKHR 243
 W+P DNVS VS+K GASP+DI+SENNYQNFATAA+NLPVLIPVT LP L +SPSDGRK
 Sbjct 181 WKPGDNVSLVSDKFGASPEDIMSENNYQNFATAANLPLVLPVRLPVLARSPSDGRKGG 240

Query 244 IGLPVIIGISLGCCTLLVVVSAILLVCVCLMKMSLNRSASSAETADKLLSGVSGYVSKPT 303
 I LPVIIGISLGCCTLLV+A+LLV V CLKMK+LNRSSAAETADKLLSGVSGYVSKPT
 Sbjct 241 IRLPVIIGISLGCCTLLVLVLAVALLVYVYCLKMKTNRSSAAETADKLLSGVSGYVSKPT 300

Query 304 MYETGAILEATMNLSEQCKIGESVYKA 330
 MYET AI+EATMNLSEQCKIGESVYKA
 Sbjct 301 MYETDAIMEATMNLSEQCKIGESVYKA 327

>**dbj|BAG85146.1| Nod factor receptor protein [Glycine soja]**

Length=327

Score = 514 bits (1324), Expect = 1e-143, Method: Compositional matrix adjust.
 Identities = 266/327 (81%), Positives = 291/327 (88%), Gaps = 1/327 (0%)

Query 5	FVSLTLGAQILYVVLMMFF-TCIEAQSQQTNGTNFSCPSNSPPSCETYVTYISQSPNFLSL	63
Sbjct 1	FPPFLPLHSQILCIVMLFSTNIVAQSQQDNRTNFSCPSDSSPSCETYVTYIAQSPNFLSL	60
Query 64	TSVSNIFDTSPSLSIARASNLQHEEDKLI PGQVLLIPVTCGCTGNRSFANISYEINQGDSF	123
T++SNIFDTSPSLSIARASNL+ +DKL+ QVLL+PVTCGCTGNRSFANISYEINQGDSF		
Sbjct 61	TNISNIFDTSPSLSIARASNLPEMDDKLKVQVLLPVTCGCTGNRSFANISYEINQGDSF	120
Query 124	YFVATTLYQNLTNWHAVMMDLNPGQLSQTLPPIGIVQVVIPLFCKCPSKNQLDRGIKYLITHV	183
YFVATT Y+NLTNW AVMDLNP LS LPIGIQVV PLFCKCPSKNQLD+ IKYLIT+V		
Sbjct 121	YFVATTSYENLTNWRAMMDLNPLVSPNKLPIGIVQVVFPLFCKCPSKNQLDKEIKYLITYV	180
Query 184	WQPNDNVSFVSNKLGASPQDILSENNYQNFATAA+NLPVLPVTP L P L +SPSDGRK	243
W+P DNVS VS+K GASP+DI+SENNYQNFATAA+NLPVLPVTP L P L +SPSDGRK		
Sbjct 181	WKPQNDNVSLVSDKFGASPEDIMSENNYQNFATAA+NLPVLPVTP L P L +SPSDGRKGG	240
Query 244	IGLPVIIGISLGCTLLVVSAILLVCVCLMKMSLNRASSAETADKLLSGVGSGYVSKPT	303
I LPVIIGISLGCTLLV+V A+LLV V CLKMK+LNRSASSAETADKLLSGVGSGYVSKPT		
Sbjct 241	IRLPVIIGISLGCTLLVLVLA VVYVYCLKMKTNRASSAETADKLLSGVGSGYVSKPT	300
Query 304	MYETGAILEATMNLSEQCKIGESVYKA 330	
MYET AI+EATMNLSEQCKIGESVYKA		
Sbjct 301	MYETDAIMEATMNLSEQCKIGESVYKA 327	

>**dbj|BAG85153.1| Nod factor receptor protein [Glycine soja]**

Length=327

Score = 514 bits (1323), Expect = 2e-143, Method: Compositional matrix adjust.
 Identities = 266/327 (81%), Positives = 290/327 (88%), Gaps = 1/327 (0%)

Query 5	FVSLTLGAQILYVVLMMFF-TCIEAQSQQTNGTNFSCPSNSPPSCETYVTYISQSPNFLSL	63
Sbjct 1	FPPFLPLHSQILCIVMLFSTNIVAQSQQDNRTNFSCPSDSSPSCETYVTYIAQSPNFLSL	60
Query 64	TSVSNIFDTSPSLSIARASNLQHEEDKLI PGQVLLIPVTCGCTGNRSFANISYEINQGDSF	123
T++SNIFDTSPSLSIARASNL+ +DKL+ QVLL+PVTCGCTGNRSFANISYEINQGDSF		
Sbjct 61	TNISNIFDTSPSLSIARASNLPEMDDKLKVQVLLPVTCGCTGNRSFANISYEINQGDSF	120
Query 124	YFVATTLYQNLTNWHAVMMDLNPGQLSQTLPPIGIVQVVIPLFCKCPSKNQLDRGIKYLITHV	183
YFVATT Y+NLTNW AVMDLNP LS LPIGIQVV PLFCKCPSKNQLD+ IKYLIT+V		
Sbjct 121	YFVATTSYENLTNWRAMMDLNPLVSPNKLPIGIVQVVFPLFCKCPSKNQLDKEIKYLITYV	180
Query 184	WQPNDNVSFVSNKLGASPQDILSENNYQNFATAA+NLPVLPVTP L P L +SPSDGRK	243
W+P DNVS VS+K GASP+DI+SENNYQNFATAA+NLPVLPVTP L P L +SPSDGRK		
Sbjct 181	WKPQNDNVSLVSDKFGASPEDIMSENNYQNFATAA+NLPVLPVTP L P L +SPSDGRKGG	240
Query 244	I GLPVIIGISLGCTLLVVSAILLVCVCLMKMSLNRASSAETADKLLSGVGSGYVSKPT	303
I LPVIIGISLGCTLLV+V A+LLV V CLKMK+LNRSASSAETADKLLSGVGSGYVSKPT		
Sbjct 241	IRLPVIIGISLGCTLLVLVLA VVYVYCLKMKTNRASSAETADKLLSGVGSGYVSKPT	300
Query 304	MYETGAILEATMNLSEQCKIGESVYKA 330	
MYET AI+EATMNLSEQCKIGESVYKA		
Sbjct 301	MYETDAIMEATMNLSEQCKIGESVYKA 327	

>**dbj|BAG85158.1| Nod factor receptor protein [Glycine max]**

Length=327

GENE ID: 100301877 nfr5a | Nod factor receptor protein [Glycine max]
 (10 or fewer PubMed links)

Score = 514 bits (1323), Expect = 2e-143, Method: Compositional matrix adjust.
 Identities = 266/327 (81%), Positives = 290/327 (88%), Gaps = 1/327 (0%)

Query 5	FVSLTLGAQILYVVLMMFF-TCIEAQSQQTNGTNFSCPSNSPPSCETYVTYISQSPNFLSL	63
Sbjct 1	FPPFLPLHSQILCIVMLFSTNIVAQSQQDNRTNFSCPSDSSPSCETYVTYIAQSPNFLSL	60
Query 64	TSVSNIFDTSPSLSIARASNLQHEEDKLI PGQVLLIPVTCGCTGNRSFANISYEINQGDSF	123
T++SNIFDTSPSLSIARASNL+ +DKL+ QVLL+PVTCGCTGNRSFANISYEINQGDSF		
Sbjct 61	TNISNIFDTSPSLSIARASNLPEMDDKLKVQVLLPVTCGCTGNRSFANISYEINQGDSF	120
Query 124	YFVATTLYQNLTNWHAVMMDLNPGQLSQTLPPIGIVQVVIPLFCKCPSKNQLDRGIKYLITHV	183
YFVATT Y+NLTNW AVMDLNP LS LPIGIQVV PLFCKCPSKNQLD+ IKYLIT+V		
Sbjct 121	YFVATTSYENLTNWRAMMDLNPLVSPNKLPIGIVQVVFPLFCKCPSKNQLDKEIKYLITYV	180
Query 184	WQPNDNVSFVSNKLGASPQDILSENNYQNFATAA+NLPVLPVTP L P L +SPSDGRK	243
W+P DNVS VS+K GASP+DI+SENNYQNFATAA+NLPVLPVTP L P L +SPSDGRK		
Sbjct 181	WKPQNDNVSLVSDKFGASPEDIMSENNYQNFATAA+NLPVLPVTP L P L +SPSDGRKGG	240
Query 244	I GLPVIIGISLGCTLLVVSAILLVCVCLMKMSLNRASSAETADKLLSGVGSGYVSKPT	303
I LPVIIGISLGCTLLV+V A+LLV V CLKMK+LNRSASSAETADKLLSGVGSGYVSKPT		
Sbjct 241	IRLPVIIGISLGCTLLVLVLA VVYVYCLKMKTNRASSAETADKLLSGVGSGYVSKPT	300
Query 304	MYETGAILEATMNLSEQCKIGESVYKA 330	
MYET AI+EATMNLSEQCKIGESVYKA		
Sbjct 301	MYETDAIMEATMNLSEQCKIGESVYKA 327	

>**dbj|BAG85172.1| Nod factor receptor protein [Glycine max]**

Length=327

Score = 514 bits (1323), Expect = 2e-143, Method: Compositional matrix adjust.
 Identities = 266/327 (81%), Positives = 290/327 (88%), Gaps = 1/327 (0%)

Query 5	FVSLTLGAQILYVVLMMFF-TCIEAQSQQTNGTNFSCPSNSPPSCETYVTYISQSPNFLSL	63
Sbjct 1	FPPFLPLHSQILCIVMLFSTNIVAQSQQDNRTNFSCPSDSSPSCETYVTYIAQSPNFLSL	60
Query 64	TSVSNIFDTSPSLSIARASNLQHEEDKLI PGQVLLIPVTCGCTGNRSFANISYEINQGDSF	123
T++SNIFDTSPSLSIARASNL+ +DKL+ QVLL+PVTCGCTGNRSFANISYEINQGDSF		

Sbjct	61	TNISNI FDTSPLSIARASNL EPMDDKL VQD QVLL VPVTCGCTGNRSFANISYE INQGDSF	120
Query	124	YFVATTLYQNLTNW HAVMDLNP GLSQFTLPIGIVQQVVIPLFC KCP SKNQLDRG IKYLITHV YFVATT Y+NLTNW AVMDLNP LS LPIGIVQQV PLFC KCP SKNQLD+ IKYLIT+V	183
Sbjct	121	YFVATT SYEN LTNWRAVM DLPVLS PKLPIGIVQQVFLFC KCP SKNQLD KEIKYLITYV	180
Query	184	WQPNDNVSFVS NKL GASP +DI LSENNY QNF TAAS NL PVLIP VTLLPDLI QSP SDGRK HR W+P DVNS VS+K GASP +DI +SENNY QNF TAAN +PVLIP LP L +SPSDGRK	243
Sbjct	181	WKPGDNVSL WS DKFGAS PED SE NN YQNF TAAN NPVLIP VTLLPDLI QSP SDGRK GG	240
Query	244	I GLPVI I G I S LG C T L L V V V S A I L L V C V C L K M K S L N R S A S S A E T A D K L L S G V G S Y V S K P T I L P V I I G I S LG C T L L V +V A+L V V C L K M K +L N R S A S S A E T A D K L L S G V G S Y V S K P T	303
Sbjct	241	I R L P V I I G I S LG C T L L V I V L A V I L V V V Y C L K M K T L N R S A S S A E T A D K L L S G V G S Y V S K P T	300
Query	304	MYETGAILEATMNL S E QCKIGESVYKA 330 MYET AI+EATMNL S E QCKIGESVYKA	
Sbjct	301	MYETDAIMEATMNL S E QCKIGESVYKA 327	

>dbj|BAG85142.1| Nod factor receptor protein [Glycine soja]
Length=327

Score	=	513 bits (1322),	Expect	=	2e-143,	Method:	Compositional matrix adjust.
Identities	=	266/327 (81%),	Positives	=	290/327 (88%),	Gaps	= 1/327 (0%)
Query	5	FVSLTLGAQILYVVIMFLF-TCIEAQSQQTNGTNFSCPSNSPPSCETVTYIISQSPNPLSL					63
Sbjct	1	F L L +QIL +V+M F T I AQSQQ N TNFSCPS+SPSCETVTYI+QSPNPLSL					
Query	64	FPFLPHSILQLCLVIMLFSTNIVQAQSQQDNRTNFSCPSDSPSCETVTYI+QSPNPLSL					60
Sbjct	61	TTSVSNIFDTSPLSIARASNLQHEEDDKL+LPGVQLLIPVTCGCTGNRSFANISYEINQGDSF					123
Query	124	T++SNI FDTSPLSIARASNL+ +DKL+ QVLL+PVTGCTGNRSFANISYEINQGDSF					
Sbjct	121	TNISNIFDTSPLSIARASNLPEMDDKLVKDVLQVLLPVPTGCTGNRSFANISYEINQGDSF					120
Query	184	YFVATTLYQNLTNWAVMDNLNPGLSQTFLPIGIQVW+PLFKCKCPSKNQLDRGIKYLITHV					183
Sbjct	181	YFVATTYSYENLTNWAVMDLNLS LPICIGQVW PLFKCKCPSKNLD+ IKYLIT+V					180
Query	244	WQPNDNVSVFSNKLQGASPQDILSENNYQGNFTAASNLPVLIPTVTLLEPDLIQSPSDGRKHR					243
Sbjct	241	W+P DNV VS+K GASP+DI+SENNYQGNFTAAN+LPVLVLPVT LP L +SPSDGRK					240
Query	304	I GLPVIIGISLGCTLLVVVSALLCVCCILMKSLNRSASSAETADKL LGSGVSGYVSKPT					303
Sbjct	301	I LPVIIIGISLGCTLLVV+A+LLV CLMRK+LNRSASSAETADKL LGSGVSGYVSKPT					300
Query	304	MYETGAIILEATMNLSEQCKIGESVYKA	330				
Sbjct	301	MYET AI+EATMNLSEQCKIGESVYKA	327				

>dbj|BAG85175.1| Nod factor receptor protein [Glycine max]
Length=327

Score	=	513 bits (1321),	Expect	=	3e-143,	Method:	Compositional matrix adjust.
Identities	=	265/327 (81%),	Positives	=	290/327 (88%),	Gaps	= 1/327 (0%)
Query	5	FVSLTIGAQILYVVIMFF-TCIEAQSQQTNGTNFSCFSNSPPSCETVTYIISQSPNFLSL	F	L L +QIL	+V+M F T I	AQSQQ N T F+CPS+SPSCETVTYIISQSPNFLSL	63
Sbjct	1	FPFLPHSILQLCLVIMLFSTNIVQAQSQQDNRTKCFDSDPSCETVTYIISQSPNFLSL					60
Query	64	TSVSNIFDTSPLSIARASNLQHEEDDKLIPGVQLLIPVTCGCTGNRSFANISYEINQGDSF	T++SNIFDTSPLSIARASNL+	+DKL+	QVLL+PVTGCTGNRSFANISYEINQGDSF		123
Sbjct	61	TNISNIFDTSPLSIARASNLPEMDDKLVDQVLVLPVFTCGCTGNRSFANISYEINQGDSF					120
Query	124	YFVATTLYQNLTNWAVMDNPLGSQFTLPIGIQVWPLFCFKCPSKNQLDRGIKYLITHV	YFVATT	Y+NLTNW	AVMDNLP LS	LPPIGIVVWPLFCFKCPSKNQLD+ IKYLIT+V	183
Sbjct	121	YFVATTSYENLTNWRAVMDNPLVSPNKLPIGIVVWPLFCFKCPSKNQLDEIKYLITYV					180
Query	184	WQPNDNVSVFSNKLGLASPQDILSENNYQGNFTAASNLPLVLIPTVTLPLDIQSPSDGRKHR	W+P	DNVS	VS+G	ASP+DI+SENNYQGNFTAADNLPLVLIPTV TL L +SFSDGRK	243
Sbjct	181	WKPQNDNVSLVSDKFGASPEDIMSENNYQGNFTAANNLPLVLIPTVRLPVLRSPSDGRKGG					240
Query	244	IGLPVIIGISLGCTLLVVSAI1LLVCVCKLMMKS1NRNSASSAETADKLLSGVSGYVSVKPT	I	LPVIIGISLGCTLLV	+V A+LL V	CLRMK+1NRNSASSAETADKLLSGVSGYVSVKPT	303
Sbjct	241	IRLPVIIGISLGCTLLVVLALVLLVYVYCLKMKT1NRNSASSAETADKLLSGVSGYVSVKPT					300
Query	304	MYETGAILEATMNLSEQCKIGESVYKA	MYET	AI+EATMNL	SEQCKIGESVYKA		330
Sbjct	301	MYETDAIMEATMNLSEQCKIGESVYKA					327

>dbj|BAG85150.1| Nod factor receptor protein [Glycine soja]
Length=327

Sbjct 301 MYET AI+EATMNLSEQCKIGESVYKA 327

>**dbj|BAG85173.1| Nod factor receptor protein [Glycine max]**
Length=327

Score = 513 bits (1320), Expect = 3e-143, Method: Compositional matrix adjust.
Identities = 265/327 (81%), Positives = 289/327 (88%), Gaps = 1/327 (0%)

Query 5	FVSLTLGAQILYYVLMFF-TCIEAQSQQTNGTNFSCPSNSPPSCETYVTYISQSPNFLSL	63
Sbjct 1	F _L L +QIL +V+M F T I AQSQQ N TNFSCPS+SPPSCETYVTYI+QSPNFLSL	60
Query 64	TSVSNIFDTSPSLSIARASNLQHEEDKLI PGQVILLIPVTCGCTGNRSFANISYEINQGDSF	123
Sbjct 61	TNISNIFDTSPSLSIARASNLQHEEDKLVKDQVLLPVTCGCTGNRSFANISYEINQGDSF	120
Query 124	YFVATTLYQNLNTNWHAVMDLNPGLSQFTLPIGIVQVVIPLFCKCP SKNQLDRGIKYLITHV	183
Sbjct 121	YFVATTLYQNLNTNWHAVMDLNPGLSQFTLPIGIVQVVIPLFCKCP SKNQLDRGIKYLITHV	180
Query 184	WQPNNDNVSFVSNKLGASPQDILSENNYQGNFTAASNLPVLI PVTLLPDLIQSPSDGRKHR	243
Sbjct 181	W _P P DNVS VS+K GASP+DI+SENNYQGNFTAANLNPVLI PVTLLPDLIQSPSDGRKHR	240
Query 244	I GLPVIIGISLGCTLLVVVSAILLVCVCLKMKSLNR SASSAETADKLLSGVGSGYVSKPT	303
Sbjct 241	I GLPVIIGISLGCTLLVVVSAILLVCVCLKMKSLNR SASSAETADKLLSGVGSGYVSKPT	300
Query 304	MYETGAILEATMNLSEQCKIGESVYKA 330	
Sbjct 301	MYETAI+EATMNLSEQCKIGESVYKA 327	

>**dbj|BAG85157.1| Nod factor receptor protein [Glycine soja]**
Length=327

Score = 513 bits (1320), Expect = 4e-143, Method: Compositional matrix adjust.
Identities = 266/327 (81%), Positives = 290/327 (88%), Gaps = 1/327 (0%)

Query 5	FVSLTLGAQILYYVLMFF-TCIEAQSQQTNGTNFSCPSNSPPSCETYVTYISQSPNFLSL	63
Sbjct 1	F _P FLPLHSQILCLVIMLFSTNIVAQSQQDNRTNFSCPSNSPPSCETYVTYISQSPNFLSL	60
Query 64	TSVSNIFDTSPSLSIARASNLQHEEDKLI PGQVILLIPVTCGCTGNRSFANISYEINQGDSF	123
Sbjct 61	TNISNIFDTSPSLSIARASNLQHEEDKLVKDQVLLPVTCGCTGNRSFANISYEINQGDSF	120
Query 124	YFVATTLYQNLNTNWHAVMDLNPGLSQFTLPIGIVQVVIPLFCKCP SKNQLDRGIKYLITHV	183
Sbjct 121	YFVATTLYQNLNTNWHAVMDLNPGLSQFTLPIGIVQVVIPLFCKCP SKNQLDRGIKYLITHV	180
Query 184	WQPNNDNVSFVSNKLGASPQDILSENNYQGNFTAASNLPVLI PVTLLPDLIQSPSDGRKHR	243
Sbjct 181	W _K PGDNVSLVSDKFGASPEDIMSENNYQGNFTAANLNPVLI PVTLLPDLIQSPSDGRKHR	240
Query 244	I GLPVIIGISLGCTLLVVVSAILLVCVCLKMKSLNR SASSAETADKLLSGVGSGYVSKPT	303
Sbjct 241	I GLPVIIGISLGCTLLVVVSAILLVCVCLKMKSLNR SASSAETADKLLSGVGSGYVSKPT	300
Query 304	MYETGAILEATMNLSEQCKIGESVYKA 330	
Sbjct 301	MYETAI+EATMNLSEQCKIGESVYKA 327	

>**dbj|BAG85176.1| Nod factor receptor protein [Glycine max]**
Length=327

Score = 511 bits (1317), Expect = 8e-143, Method: Compositional matrix adjust.
Identities = 265/327 (81%), Positives = 290/327 (88%), Gaps = 1/327 (0%)

Query 5	FVSLTLGAQILYYVLMFF-TCIEAQSQQTNGTNFSCPSNSPPSCETYVTYISQSPNFLSL	63
Sbjct 1	F _P FLPLHSQILCLVIMLFSTNIVAQSQQDNRTNFSCPSNSPPSCETYVTYISQSPNFLSL	60
Query 64	TSVSNIFDTSPSLSIARASNLQHEEDKLI PGQVILLIPVTCGCTGNRSFANISYEINQGDSF	123
Sbjct 61	TNISNIFDTSPSLSIARASNLQHEEDKLVKDQVLLPVTCGCTGNRSFANISYEINQGDSF	120
Query 124	YFVATTLYQNLNTNWHAVMDLNPGLSQFTLPIGIVQVVIPLFCKCP SKNQLDRGIKYLITHV	183
Sbjct 121	YFVATTLYQNLNTNWHAVMDLNPGLSQFTLPIGIVQVVIPLFCKCP SKNQLDRGIKYLITHV	180
Query 184	WQPNNDNVSFVSNKLGASPQDILSENNYQGNFTAASNLPVLI PVTLLPDLIQSPSDGRKHR	243
Sbjct 181	W _K PGDNVSLVSDKFGASPEDIMSENNYQGNFTAANLNPVLI PVTLLPDLIQSPSDGRKHR	240
Query 244	I GLPVIIGISLGCTLLVVVSAILLVCVCLKMKSLNR SASSAETADKLLSGVGSGYVSKPT	303
Sbjct 241	I GLPVIIGISLGCTLLVVVSAILLVCVCLKMKSLNR SASSAETADKLLSGVGSGYVSKPT	300
Query 304	MYETGAILEATMNLSEQCKIGESVYKA 330	
Sbjct 301	MYETAI+EATMNLSEQCKIGESVYKA 327	

>**dbj|BAG85155.1| Nod factor receptor protein [Glycine soja]**
Length=327

Score = 511 bits (1316), Expect = 1e-142, Method: Compositional matrix adjust.
Identities = 265/327 (81%), Positives = 289/327 (88%), Gaps = 1/327 (0%)

Query 5	FVSLTLGAQILYYVLMFF-TCIEAQSQQTNGTNFSCPSNSPPSCETYVTYISQSPNFLSL	63
Sbjct 1	F _P FLPLHSQILCLVIMLFSTNIVAQSQQDNRTNFSCPSNSPPSCETYVTYISQSPNFLSL	60
Query 64	TSVSNIFDTSPSLSIARASNLQHEEDKLI PGQVILLIPVTCGCTGNRSFANISYEINQGDSF	123

Sbjct	61	T++SNIFDTSPLSIARASNL+ +DKL+ QVLL+PVT CGCTGNRSFANISYEINQGDSF TNISNIFDTSPLSIARASNL EPMDDKLVKDQVLLPVFTCGCTGNRSFANISYEINQGDSF	120
Query	124	YFVATTLYQNLTNWAVMDLNPLQLSQQTLPIGIQVVIPLFCPKCPSKNQLDRGKYLITYHV YFVAT Y+NLTNW AVMDLNPL P LPIQIV PLFCPKCPSKNQLD+ IKYLIT+V	183
Sbjct	121	YFVATPSYENLTNWRAVMDLNPVLSPNKLPIGIVQEFPFLFCPKCPSKNQLDEIKYLITYV	180
Query	184	WQPNDNVSFVSNKLGASPQDILSENNYQGQNFTAASNLPVLI PVTLLPDLIQSPSDGRKHR W+P DNVS VS+k GASP+DI+SENNYQGQNFTAALNLPVLI PVTLPRLPVLA RSPSDGRKG	243
Sbjct	181	WKPQDNVSLVSDKFAGSPEDIMSENNYQGQNFTAANNLPVLI PVTLPRLPVLA RSPSDGRKG	240
Query	244	I GLPVIIIGISLGCTLLVVSA ILLVCVCLMKMSLNRSASSAETADKL LSGVSGYVSKPT I LPVIIIGISLGCTLLVV A+LLV V CLMKM+LNRSASSAETADKL LSGVSGYVSKPT	303
Sbjct	241	IIRLPVIIIGISLGCTLLVLVLA VLLVVY CLMKMTLNRSASSAETADKL LSGVSGYVSKPT	300
Query	304	MYETGAILEATMNLSEQC KIGESVYKA 330 MYET AI+EATMNLSEQC KIGESVYKA	330
Sbjct	301	MYETDAIMEATMNLSEQC KIGESVYKA 327	327

>dbj|BAG85163.1| Nod factor receptor protein [Glycine max]
Length=327

Score =	511 bits (1315),	Expect =	2e-142,	Method:	Compositional matrix adjust.
Identities =	265/327 (81%),	Positives =	289/327 (88%),	Gaps =	1/327 (0%)
Query 5	FVSLTGLAQIYVVIMFF-TCIEAQSQQTNTFSCPSNSPPSCETTYVTYISQSPNPLSL	63			
Sbjct 1	F L L +QIL +V+M F T I AQSQQ N TNFSCPS+SP SCETVY YI+QSPNPLSL	60			
Query 64	TSVSNIFDTSPLSIARASNLQHEEDDKLIPGQVLLIPVTCGCTGNRSFANISYEINQGDSF	123			
Sbjct 61	T+ +SNI DFTSPLSIARASNL+ +DKL+ QVLL+PVTGCGTGNRSFANISYEINQGDSF	120			
Query 124	YFVATTLYQNLNTNWAVMDLNPGLSQFTLPIGIVVPLFCKCPSKNQLDRGIKYLITHV	183			
Sbjct 121	YFVATTYSYENLTNWRAVMMDLNPKLPIGIVVPLFCKCPSKNQLDKEIKYLITYV	180			
Query 184	WQPNDNVSVFSNKLGASPQDILSENNYQGQFTAASNLPLVLIPTVTLPLDIQSPSDGRKHR	243			
Sbjct 181	WKPQNDVSVLSVDKGASPDEIMSENYYQGQFTAANNLPLVLIPTVTRLVLARSPLSDGRKGG	240			
Query 244	IGLPVIIGISLGCTLVVVSAILLVCCCLKMKMSLNRSASSAETADKLLSGVSGYVSKPT	303			
Sbjct 241	I LPVIIIGISLGCTLV+V A+LL V CLKMK+LNRSASSAETADKLLSGVSGYVSKPT	300			
Query 304	MYETGAIILEATMNLSEQCKIGESVYKA	330			
Sbjct 301	MYET AI+EATMNLSEQCKIGESVYKA	327			

>dbj|BAG85154.1| Nod factor receptor protein [Glycine soja]
Length=327

Score =	509 bits (1311),	Expect =	4e-142,	Method:	Compositional matrix adjust.
Identities =	264/327 (80%),	Positives =	289/327 (88%),	Gaps =	1/327 (0%)
Query 5	FVSSLTGLAQIYLGVVLMFF-TCIEAQSQQTNTNFSCPSNSPSCETVYTVYIQSQSPNFLSL	63			
Sbjct 1	F L L +QIL +V+M F T I AQSQQ N TNFSCPS+SPSCTEVTVYI+QSQSPNFLSL	60			
Query 64	TSVSNIFDTSPLSIARASNLQHEEDDKLIPGQVLLIPVTCGCTGNRSFANISYEINQGDSF	123			
Sbjct 61	T++SNI DFTSPLSIARASNL+ +DKL+ QVLL+PVTCGCTGNRSFANISYEINQGDSF	120			
Query 124	YFVATTLYQNLNTNWAVMDLNPGLSQFTLPIQVVIPLFKCPSPKNQLDRGIKYLITHV	183			
Sbjct 121	YFVATTYSYENLTNWRAVMMDLNQVLPVTCGCTGNRSFANISYEINQGDSF	180			
Query 184	WQPNDNVSVFSNKLQASPQDILOSENNYQGNFTAASNLQVLPVTLPLDIQSPSDGRKHR	243			
Sbjct 181	W+P D+VS VS+K GASP+DI+SENNY QNFTAA+NLQVLPVTLPLDIQSPSDGRK	240			
Query 244	IGLPVIIIGISLGCTLLVVSAI1LLVCVCCCLKMKSLNRSASSAETADKLLSGVSGYVSKPT	303			
Sbjct 241	I LPVIIIGISLGCTLLVV+A+LLV V CLKMK+LNRSASSAETADKLLSGVSGYVSKPT	300			
Query 304	MYETGAILEATMNLSEQCKIGESVYKA	330			
Sbjct 301	MYETAI+EATMNLSEQCKIGESVYKA	327			

>dbj|BAG85169.1| Nod factor receptor protein [Glycine max]
Length=327

Score =	507 bits (1305),	Expect =	2e-141,	Method:	Compositional matrix adjust.
Identities =	264/327 (80%),	Positives =	289/327 (88%),	Gaps =	1/327 (0%)
Query	5	FVSLTILGAQILYVVLMFF-TCIEAQSQQTNGTNFSCPSNSPSCETVVTYIQSQSPNFLSL	63		
Sbjct	1	F L L +QIL +V+M F T I AQSQQ N TNFSCPS+SPPSCETVVTYI+QSPNPFLSL	60		
Query	64	TSVSNI FDTSPLSIARASNLIQHEEDDKLIPGVQLLIPVTCGCTGNRSFANISYEINQGDSF	123		
Sbjct	61	T++SNI FDTSPLSIARASNLI+ +DKL+ QVLL+PVTGCTGNRSFANISYEINQGDSF	120		
Query	124	YFVATTLYQNLTNWAVMDLNPGLSQFTLPIGIVQVVIPLFKCPSPKNQLDRLGIKYLITHV	183		
Sbjct	121	YFVATT Y+NLTN AVMDLNPGLSQFTLPIGIVQVVIPLFC+CPSKNQLD+ IKYLIT+V	180		
Query	184	WQPNDNVSVFSNKLGASPQDILENSENNYQGNFTAASNLPVLIPTVTLBDLIQSPSDGRKHR	243		
Sbjct	181	W+P DNVS VS+K GASP+DI+SENNYQGNFTAANLPVLIPVTLBDLIQSPSDGRKGG	240		
Query	244	IGLPVIIIGISLGCTLLVVVAIALLVCCVCLKMKSLSRNASSAETADKLLSGVSGYVSKPT	303		
Sbjct	241	I LPVIIIGISLGCTLLVVVAI ALLV V CLMKMSLSRNASSAETADKLLSGVSGYVSKPT	300		

Query 304 MYETGAILEATMNLSEQCKIGESVYKA 330
 Sbjct 301 MYETDAIMEATMNLSEQCKIGESVYKA 327

>dbj|BAG85166.1| Nod factor receptor protein [Glycine max]
 Length=327

Score = 501 bits (1291), Expect = 9e-140, Method: Compositional matrix adjust.
 Identities = 260/324 (80%), Positives = 286/324 (88%), Gaps = 1/324 (0%)

Query 5 FVSITLGAQI LYVVLMLFF-TCIAQSQQTNGTNFSCPSNSPPSCETYVTYISQSPNFLSL 63
 F L +QIL +V+M F T I AQSQQ N TMFSCPS+SPPSCETYVTYI+QSPNFLSL
 Sbjct 1 FPFPLHSQLICLIVMLFSTNIVAQSQDNRNTFSCPSDPPSCETYVTYIAQSPNFLSL 60

Query 64 TSVSNI FDTSPSPLSIARASNLQHEEDKLI PGQVLLIPVTCGCTGNRSFANISYEINQGDSF 123
 T++SNIFDTSPLSIARASNL+ +DKL+ QVLL+PVTGCTGNRSFANISYEINQGDSF
 Sbjct 61 TNISNIFDTSPLSIARASNLPEMDDKLKVQDQVLLPVTCGCTGNRSFANISYEINQGDSF 120

Query 124 YFVATTLYQNLTNWHAVMMDLNPGQLSQFTLPIGIQVVIPLFCKCPSKNQLDRGIKYLITHV 183
 YFVATT Y+NLTNW AVMDLN P LS LPIGIQVV PLFCKCP SKNQLD+ I+YLIT+V
 Sbjct 121 YFVATTYSENLTNWRAVMMDLNPGQLSQFTLPIGIQVVPLFCKCP SKNQLDKEIRYLITYV 180

Query 184 WQPNDNVSFVSNKLGA SPQDILSENNYQGNFTAASNLPVLPVTL PDLIQSPSPDGRKHR 243
 W+P DVNS VS+K GAS P+DI+SENNYQGNFTA+NLPVLPV LP L +SPSDGRK
 Sbjct 181 WKPGDNVSLVSDKFGAS PEDIMSENNYQGNFTAANNLPVLPVTRLPVLRSPSDGRKGG 240

Query 244 IGLPVIIGISLGCTLLVVSAI LVCVCLMKMSLNRSASSAETADKL LSGVSGYVSKPT 303
 I GLPVIIGISLGCTLLV V+A+LL V CLMK+LNRSASSAE ADKL LSGVSGYVSKPT+PT
 Sbjct 241 IRLPVIIGISLGCTLLV LVA L VVYVYCLMKM TLNRSSASSAENADKL LSGVSGYVSKPT 300

Query 304 MYETGAILEATMNLSEQCKIGESV 327
 MYET AI+EATMNLSEQCKIG SV
 Sbjct 301 MYETDAIMEATMNLSEQCKIGISV 324

>emb|CAO02936.1| LysM-domain containing receptor-like kinase [Medicago truncatula]
 var. truncatula
 Length=349

Score = 482 bits (1240), Expect = 8e-134, Method: Compositional matrix adjust.
 Identities = 238/351 (67%), Positives = 288/351 (82%), Gaps = 4/351 (1%)

Query 53 YISQSPNFLSLTSVSNIFDTSPSPLSIARASNLQHEEDKLI PGQVLLIPVTCGCTGNRSFAN 112
 Y +QSPNFLSL++S+IF+ SPL IA+ASN++ E+ KLI P Q+LL+PVTGCT N SFAN
 Sbjct 1 YRAQSPNFLSLNSIDFNLSPLRIAKASNIEADEDKKLIPDQLLL PVTCGCTKNHSFAN 60

Query 113 ISYEINQGDSFYFVATTLYQNLTNWHAVMMDLNPGQLSQFTLPIGIQVVIPLFCKCP SKNQL 172
 I+Y I QGD+F+ ++ T YQNLTN+ + NP LS LP+ +V +PLFCKCP SKNQL
 Sbjct 61 ITYSIKQGDNNFFILSITSYQNLTYLEFKFNFPNLSPTLLPLDTKVSVPLFCKCP SKNQL 120

Query 173 DRGIKYLITHW WQPNDNVSFVSNKLGA SPQDILSENNYQGNFTAASNLPVLPVTL PDL 232
 ++GIKYLIT+VWQ NDNV+ VS+K GAS ++I+ENN+ NFTA++N VLIPV LP L
 Sbjct 121 NKGIKYLITYVWQDNDNVTLVSSKGASQVEMLAENN--NFTASTNRSVLIPVTSPLPKL 178

Query 233 IQSPSPDGRKHRI- GLPVIIGISLGCTLLVVSAI LVCVCLMKMSLNRSASSAETADKL 291
 Q S+GRK L +IIGISLG +V + LV V CLMK LNRS SS+ETADKL
 Sbjct 179 DQPSSNGRKSSSQNLALIIGISLGS AFFILVLTSLVYVYCLMKR LNRSTSSSETADKL 238

Query 292 LSGVSGYVSKPTM YETGAILEATMNLSEQCKIGESVYKANIEGKVLAVKRFKEDVTEELK 351
 LSGVSGYVSKPTM YE AI+E TMNLS+ CKIGESVYKANI+G+VLA VK+ K+D +EELK
 Sbjct 239 LSGVSGYVSKPTM YE IDAIMEGTNNLSDNCKIGESVYKANIDGRVLAVKKIKKDASEELK 298

Query 352 ILQKVN HGNLVKL MGVS SDNGNC FV VY EYAENG SLEE WLFAKC SETS NS 402
 ILQKVN HGNLVKL MGVS SDNGNC FV VY EYAENG SLEE WLFS +S S+TS NS
 Sbjct 299 ILQKVN HGNLVKL MGVS SDNGNC FV VY EYAENG SLEE WLFS -SKTS NS 348

>emb|CAO02948.1| LysM-domain containing receptor-like kinase [Medicago truncatula]
 var. truncatula
 Length=337

Score = 465 bits (1197), Expect = 7e-129, Method: Compositional matrix adjust.
 Identities = 228/339 (67%), Positives = 275/339 (81%), Gaps = 3/339 (0%)

Query 48 ETYYT YISQSPNFLSLTSVSNIFDTSPSPLSIARASNLQHEEDKLI PGQVLLIPVTCGCTGN 107
 ETYY Y +QSPNFLSL++S+IF+ SPL IA+ASN++ E+ KLI P Q+LL+PVTGCT N
 Sbjct 1 ETYYVAYRAQSPNFLSLNSIDFNLSPLRIAKASNIEADEDKKLIPDQLLL PVTCGCTKN 60

Query 108 RSFANISYEINQGDSFYFVATTLYQNLTNWHAVMMDLNPGQLSQFTLPIGIQVVIPLFCKCP 167
 SFANI+Y I QGD+F+ ++ T YQNLTN+ + NP LS LP+ +V +PLFCKCP
 Sbjct 61 HSFANITYS IKQGDNNFFILSITSYQNLTYLEFKFNFPNLSPTLLPLDTKVSVPLFCKCP 120

Query 168 SKNQLDRGIKYLITHW WQPNDNVSFVSNKLGA SPQDILSENNYQGNFTAASNLPVLPV 227
 SKNQL+ +GIKYLIT+VWQ NDNV+ VS+K GAS ++I+ENN+ NFTA++N VLIPV
 Sbjct 121 SKNQLNKIGYLYT VVWQDNDNVTLVSSKGASQVEMLAENN--NFTASTNRSVLIPV 178

Query 228 LLPPLI QSPSPDGRKHRI- GLPVIIGISLGCTLLVVSAI LVCVCLMKMSLNRSASSA 286
 LP L Q S+GRK L +IIGISLG +V + LV V CLMK LNRS SS+E
 Sbjct 179 SLPKLDQPSNGRKSSSQNLALIIGISLGS AFFILVLTSLVYVYCLMKR LNRSTSSSE 238

Query 287 TADKL LSGVSGYVSKPTM YETGAILEATMNLSEQCKIGESVYKANIEGKVLAVKRFKEDV 346
 TADKL LSGVSGYVSKPTM YE AI+E T NLS+ CKIGESVYKANI+G+VLA VK+ K+D
 Sbjct 239 TADKL LSGVSGYVSKPTM YE IDAIMEGTNNLSDNCKIGESVYKANIDGRVLAVKKIKKD 298

Query 347 TEELKILQKVN HGNLVKL MGVS SDNGNC FV VY EYAENG 385
 +EELKILQKVN HGNLVKL MGVS SDNGNC FV VY EYAENG
 Sbjct 299 SEELKILQKVN HGNLVKL MGVS SDNGNC FV VY EYAENG 337

>emb|CAO02942.1| LysM-domain containing receptor-like kinase [Medicago truncatula]
 var. truncatula
 Length=334

Score = 462 bits (1190), Expect = 4e-128, Method: Compositional matrix adjust.
 Identities = 227/336 (67%), Positives = 274/336 (81%), Gaps = 3/336 (0%)

Query 53 YISQSPNFLSLTSVSNIFDTSPSPLSIARASNLQHEEDKLI PGQVLLIPVTCGCTGNRSFAN 112

Sbjct 1 Y +QSPNFLSL+++S+IF+ SPL IA+ASN++ E+ KLIP Q+LL+PVTCGCT N SFAN
YRAQSPNFLSLSNISDIFNLSPRIAKASNIEADKKLIPDQLLVPVTCGCTKNHSFAN 60

Query 113 ISYEINQGDSFYFVATTLYQNLTNWHAVMIDLNPGLSQFTLPIGIQVVIPLFCKCP SKNQL 172
I+Y I QGD+F+ ++ T YQNLTN+ + NP LS LP+ +V +PLFCKCP SKNQL 120

Sbjct 61 ITYSIKQGDNFFILSITSYQNLTNYLEFKNFNPNSPTLLPLDTKVSPLFCKCP SKNQL 120

Query 173 DRGIKYLITHWQPNDNVSFVNKL GAS PQDI LSENNYQGNFTAASNL PVLIPVTLLPDL 232
++GIKYLIT+VWQ NDNV+ VS+K GAS ++I+ENN+ NFTA++N VLIPVT LP L 232

Sbjct 121 NKGKYLITYVWQDNNDNVTLVSSKFGASQVEMLAENN--NFTASTNRSVLIPVTS LPKL 178

Query 233 IQSPSDGRKHRI-GLPVIIGISLGCTLLVVVAI LVCVCC LKMKS LNR SASSAETADKL 291
Q S+GRK L +IIGISLG +V + LV V CLMK LNRS SS+ETADKL 291

Sbjct 179 DQPSSNGRKSSQNLALIIIGISLGS AFFILVLTLSLVVYCLRMKRLNRSTSSSETADKL 238

Query 292 LSGVSGYVSKP TMYETGAILEATMNLSEQCKIGESVYKANIEGKVLA V KRFKEDDVTEELK 351
LSGVSGYVSKP TMYE AI+E TMNL S+ CKIGESVYKANI+G+VLA V K+D +EELK 351

Sbjct 239 LSGVSGYVSKP TMYEIDAIMEGT MNLSDNC KIGESVYKANIDGRV LA V KIKKDASEELK 298

Query 352 ILQKVN HGNL VKL MGVSS DNDGNCF+VVEYAENGSL 387
ILQKVN HGNL VKL MGVSS DNDGNCF+VVEYAENGSL 387

Sbjct 299 ILQKVN HGNL VKL MGVSS DNDGNCFLVYBYAENGSL 334

>emb|CAO02960.1| LysM-domain containing receptor-like kinase [Medicago truncatula]
var. truncatula]
Length=333

Score = 458 bits (1179), Expect = 9e-127, Method: Compositional matrix adjust.
Identities = 225/335 (67%), Positives = 272/335 (81%), Gaps = 3/335 (0%)

Query 53 YISQSPNFLSLTSVSNIFDTPLSIARASNLQHEEDKLIPGQVLLIPVTCGCTGNRSEFAN 112
Y+QSPNFLSL+++S+IF+ SPL IA+ASN++ E+ KLIP Q+LL+PVTCGCT N SFAN 60

Sbjct 1 YRAQSPNFLSLSNISDIFNLSPRIAKASNIEADKKLIPDQLLVPVTCGCTKNHSFAN 60

Query 113 ISYEINQGDSFYFVATTLYQNLTNWHAVMIDLNPGLSQFTLPIGIQVVIPLFCKCP SKNQL 172
I+Y I QGD+F+ ++ T YQNLTN+ + NP LS LP+ +V +PLFCKCP SKNQL 120

Sbjct 61 ITYSIKQGDNFFILSITSYQNLTNYLEFKNFNPNSPTLLPLDTKVSPLFCKCP SKNQL 120

Query 173 DRGIKYLITHWQPNDNVSFVNKL GAS PQDI LSENNYQGNFTAASNL PVLIPVTLLPDL 232
++GIKYLIT+VWQ NDNV+ VS+K GAS ++I+ENN+ NFTA++N VLIPVT LP L 232

Sbjct 121 NKGKYLITYVWQDNNDNVTLVSSKFGASQVEMLAENN--NFTASTNRSVLIPVTS LPKL 178

Query 233 IQSPSDGRKHRI-GLPVIIGISLGCTLLVVVAI LVCVCC LKMKS LNR SASSAETADKL 291
Q S+GRK L +IIGISLG +V + LV V CLMK LNRS SS+ETADKL 291

Sbjct 179 DQPSSNGRKSSQNLALIIIGISLGS AFFILVLTLSLVVYCLRMKRLNRSTSSSETADKL 238

Query 292 LSGVSGYVSKP TMYETGAILEATMNLSEQCKIGESVYKANIEGKVLA V KRFKEDDVTEELK 351
LSGVSGYVSKP TMYE AI+E TMNL S+ CKIGESVYKANI+G+VLA V K+D +EELK 351

Sbjct 239 LSGVSGYVSKP TMYEIDAIMEGT MNLSDNC KIGESVYKANIDGRV LA V KIKKDASEELK 298

Query 352 ILQKVN HGNL VKL MGVSS DNDGNCF+VVEYAENGSL 386
ILQKVN HGNL VKL MGVSS DNDGNCF+VVEYAENGSL 386

Sbjct 299 ILQKVN HGNL VKL MGVSS DNDGNCFLVYBYAENGSL 333

>gb|AAM19130.1|AC103891_10 Putative protein kinase [Oryza sativa Japonica Group]
>gb|ABF94815.1| Protein kinase domain containing protein [Oryza sativa (japonica cultivar-group)]
>gb|EAZ26175.1| hypothetical protein OsJ_10042 [Oryza sativa Japonica Group]
Length=624

Score = 426 bits (1095), Expect = 5e-117, Method: Compositional matrix adjust.
Identities = 249/598 (41%), Positives = 357/598 (59%), Gaps = 45/598 (7%)

Query 11 GAQILYVVL MF-FTCIEAQSSQT-NGTNFSCPSNSPPSCETVYIYISQSPNFLSLTVSN 68
G IL VV+ F EA + T F+C ++P C+T+V Y +QSP FL L ++S+
Sbjct 5 GLCILAVVIAFQLAGGEAVTDATARARRFACNVSA --CDTFVYVRTQSPGFLD LGNISD 62

Query 69 IFDTSPLSIARASNLQHEEDKLIPGQVLLIPVTCGCTGNRFSAN ISYEINQGDSFYFVAT 128
+F S IA L E+ L+PGQ LL+PV CGCT RSFA N++Y I D+F+ +A
Sbjct 63 LFVGSRALIASANKLTTEDGVLLPGQPLLVPVKCGCTGARSFANV TYFIRPRDTFFGLAV 122

Query 129 TLYQNLTNWHAVMIDLNPGLSQFTLPIGIQVVIPLFCKCP SKNQL DRGIKYLITHWQPND 188
T ++NLT++ V +LNP L +VV+PLFC+C P++ +L G + L+T+VWQP D 188

Sbjct 123 TAFENLTD FV LVEELNPAAEATRLEPWQE VVVVLF C RCP T REELSAGS RLLV TYVWQP GD 182

Query 189 NVSFVSNKL GAS PQDI LSENNYQGNFTAASNL PVLIPVTLLPDL-----IQSPSDGR 241
+VS VS + AS +I + N N T A+ PV LIPV+ P I + K
Sbjct 183 DSVVSALMN ASAANIA ASNGVAGNSTFATGQFVLPV SQPPRFPLTYGAIAADPGAGK 242

Query 242 HRIGLPVIIGISLGCTLLVVVAI LVCVCC LKM-----KSLNRSAS 283
HR G +I+ S + V A+ L + + KSLNRSAS
Sbjct 243 HRHG-IIIVATSIAGSF--VACAVLCTAI LAYRRYRK KAPVPKH VSPKLSWT KSLNRFDS 298

Query 284 SAETA-----DKLLSGVSGYVSKP TMYETGAILEATMNLSEQCKIGESVYKANIEGKV L 337
++ A DKL+ VS ++ KP ++ +I+EATMNL E QCK+G S Y+AN+E +V
Sbjct 299 NSSIARMINGGD KLLTSV SQFIDKPII FFREEEIMATMNL DEQCKLGSSYYRANLEREVF 358

Query 338 AVKRFKEDDVTEELK I LQKVN HGNL VKL MGVSS DNDGN -CFV VYBYAENGSL EEWLF AKSC 396
AVK K +V EL+ ++Q VNH NL KL G+S DG+ F+VYE+AE GSL++WL+ K
Sbjct 359 AVKPAKGNVAGE L RMMQMVN HANLTKLAGISIGADGDY AFVYEEFAEKGS LD KWLY QRP 418

Query 397 SETSNR--TSLTW CQRISIAVDVSMGLQYMHEHAYPRI VHDITSSNILLDSNF KAKIA 454
+S +L+W QR+ IA+DV+ GL Y+HEH P +VH D+ + NILL + F+AK++
Sbjct 419 CSQPSSSSVATL SDW QRLG D VHL WANG L HBT QPSMVH D VRARNILLTAGFRAKLS 478

Query 455 NFSMAR--TFTNPMSKIDVFAFGVVLIELLTGRKAMTTKENG EVVMI LWKDI WKIFDQ-E 511
NFS+A+ + + DVFAFG+ +ELL+GR+A+ + E+ ML +I + D
Sbjct 479 NFSLAKPAAMV DAAATSSDVFAFGLL LE LLSG RRAVEARVG EIGML RT EIRT VLDAGG 538

Query 512 ENREERL R KWMDP KLDNYY PIDY ALASLAV NCTADK SLSR PTIA EIVL SLSLL TQP 569
+ R +L R KWMDP L Y +D ALSLA +A CT + + RP +AEI SLS+L QP
Sbjct 539 DKRAAKL R KWMDP TLG GEYGVDAAL SLAG MARACTEEDA ARPKMAEIA FSLV LGQP 596

>ref|XP_002468236.1| hypothetical protein SORBIDRAFT_01g042230 [Sorghum bicolor]

gb|EER95234.1| hypothetical protein SORBIDRAFT_01g042230 [Sorghum bicolor]
Length=631

Gene ID: 8085264 SORBIDRAFT_01g042230 | hypothetical protein [Sorghum bicolor]
(10 or fewer PubMed links)

Score = 426 bits (1094), Expect = 5e-117, Method: Compositional matrix adjust.
Identities = 245/592 (41%), Positives = 350/592 (59%), Gaps = 56/592 (9%)

Query 28	QSQQTNGTNFSCP-----SNSPPSCETYVTYISQSPNFLSITSVSNIFDTSPLSIARA	80
Sbjct 18	Q+ + TN++ P S+SPP C+TYV Y +QSP + L S+S+F TS IA A QAGAQDNTNTYTVPAQFACNVSSSSPCDTYVVYRTQSPGYQDLGSISDLFGTSQARIASA	77
Query 81	SNLQHEEDKLIPIGQVLLIPVTCGCTGNRSFANISYEINQGDSFYFVATTLYQNLTNWHA	139
Sbjct 78	+ L E+ L PGQ LL+PV+ CGCTG SFAN+Y I QGD+F+ +A Y+NLT + NGLSSSEDGVLPQGPPLVPSVKCGCTGGWSFANVTYPIRQGDTFFNLARVSYENLTLYQL	137
Query 140	VMDLNPGLSQFTLPIGIQVVIPLFCKCPSKNQLDRGIKYLYTHWQPNNDNSVFSNLGA	199
Sbjct 138	+ LNP + L +G +V +PLFC+CP+ + IT+VWQ D +S VS + IQNINPRSVPTSLQVGQEVTVPLFCRCPAPAERSS----FITYVWQAGDTMSQVSKLMT	193
Query 200	SPQDILSENNEYGQNFTAAS-NLPVLIPTVLLPDL-----IQSPSDGRKRHIGLPVIIIGI	252
Sbjct 194	+ I NN + +AS P+LIPV P L S DG+ VIIG TEDEIAEANNVTSSSASASLVGQPMILIPVQQRPLPPLHYAASAGDGKSRWRRRAVIIGA	253
Query 253	SLGCTLLVVVAIALLVCVCCLK-----MKSLNRSASSAE-----	286
Sbjct 254	S+ + VV A L V + L+ M+ +R A + + SVSGS--VVALAALFVAILALRRYRKPKSMRLGSRAVNTKLTWSRNQFGHDSSNSFAHM	311
Query 287	---TADKLLSGVSGYVSKPTMYETGAILEATMNLSEQCKIGESVYKANIEGKVLAVERFK	343
Sbjct 312	KLL+GVS ++ KP ++ I-EATMNL E+CKIG + Y+A ++G+V AVK K MKLGKGKLLTGVSFIDKPIIFLEEEIMEATMNLDERCKIGSTYYRAKLDGEFAVAKPAK	371
Query 344	EDVTEELKILQKVNHHGNLNVKLMGVSSDNDGN-CFVYYEYAENGSLLEEWLFAKSCSETSNS	402
Sbjct 372	DV+ ELK++Q VNH NL+KL G+S DG+ F+VYE+AE GSL++WL+ K S +S GDVSAELKMMQMVNHNHLKLAGISIGTDGDYAFLVYEFAEKGSLDKWLYQKPPSALPSS	431
Query 403	R-----TSLTWCQRISIAVDVSMGLQYMHEAYPRIVHRDITSSNILLDSNFKAKIANFSM	458
Sbjct 432	+L+W QR+SIA+DV+ GL YMHEH P +VH DI + NILL + F+ K+ FS+ SCTVTATLSWQQLRSLIAVDVANGLLYMEHTQPSMVHGDIRARNILLAEFRKISGFSL	491
Query 459	AR-TFTNPMMSKIDVFAFGVVLIELLTGRKAMTTKENGEVVMILWKDIWKFQDQEENREER	517
Sbjct 492	At + + DVFAFG++L+ELL+GR+AM + E+ MIW++I + D + RE + AKPATADAATSSDVFAFGLLLLELLSGRRAMEARVGSEIGMLWREIRGVLDAGDKREAK	551
Query 518	LRKWMMDPKLDNYYPIDYALSLASLAVNCTADKSLSRPTIAIEIVLSSLTQP	569
Sbjct 552	L KWMMPD L + Y +D ALSLA +A CT D + RP + E+V SLS+L QP LGKWMMDPALGSEYHMDAALSAGMARACTEDDAARRPNMTEVVFSLSLVQP	603

>gb|EAY89155.1| hypothetical protein OsI_10648 [Oryza sativa Indica Group]
Length=624

Score = 424 bits (1090), Expect = 2e-116, Method: Compositional matrix adjust.
Identities = 248/598 (41%), Positives = 357/598 (59%), Gaps = 45/598 (7%)

Query 11	GAQILYVVLMF-FTCIEAQSSQQT-NGTNFSCPSNSPPSCETYVTYISQSPNFLSITSVSN	68
Sbjct 5	G IL VV+ F +A + T F+C ++P C+T+V Y +QSP FL L ++S+ GLCILAVVIAFQLAGGQAVTDATARARRFACNVSA--CDTFVYRTQSPGFLDGNISD	62
Query 69	IDFTSPLSIARASNQHQEEDKLIPIGQVLLIPVTCGCTGNRSFANISYEINQGDSFYFVAT	128
Sbjct 63	+F S IA A + L E+ L+PGQ LL+PV CGCTG RSFAN+Y I D+F+ +A LFGVSRALIASANKLTTEDGVLPQGPPLVVKCGCTGARSFANVTYPIRPRDTFFGLAV	122
Query 129	TLYQNLTNWHAVMDLNPGLSQFTLPIGIQVVIPLFCKCPSKNQLDRGIKYLYTHWQPN	188
Sbjct 123	T++NLT++ V +LNP L +VV+PLFC+CP++ +L G + L+VWQP D TAFENLTDVFVLEELNPAAEATRLEPWQEVVVFLFCRCPTREELSAGSRLLVWQPGD	182
Query 189	NVSFSNKLGSPQDILSENNEYGQNFTAASNLVPLIPVTLPPDL-----IQSPSDGRK	241
Sbjct 183	+VS VS + AS +I + N N T A+ PVLPV+ P I + K DVSVSALMNAAAANIAASNGVAGNSTFATGQPVLIPVSPQPPRFPLTYGAIADPGAGK	242
Query 242	HRIGLPVIIGISLGCTLLVVVAIALLVCVCCLK-----MKSLNRSAS	283
Sbjct 243	HR G +I+ St + V A+L + + HRHG--IIIVATSIAGSF--VACAVLCTIALYRKYKAPVPHVSPKLSWTKSLNRFD	298
Query 284	SAETA-----DKLLSGVSGYVSKPTMYETGAILEATMNLSEQCKIGESVYKANIEGKVL	337
Sbjct 299	++ A DKL+ VS ++ KP ++ I+EATMNL EQCK+G S Y+AN+E +V NSSIARMINGDKL LTSVSQFIDKPIIFREEEIMEATMNLDEQCKLGSSYYRANLEREVF	358
Query 338	AVKRFKEDVTEELKILQKVNHHGNLNVKLMGVSSDNDGN-CFVYYEYAENGSLLEEWLFAKSC	396
Sbjct 359	AVK K +V EL++Q VNH NL KL G+S DG+ F+VYE+AE GSL++WL+ K AVPKAKGNVAGELRMMQMVNHNHLKLAGISIGADGDYAFLVYEFAEKGSLDKWLYQKPP	418
Query 397	SETNSNR--TSLTWCQRISIAVDVSMGLQYMHEAYPRIVHRDITSSNILLDSNFKAKIA	454
Sbjct 419	+S +L+W QR+ IA+DV+ GL Y+HEH P +VH D+ + NILL + F+AK++ CSQPSSSSVATLSWDQRQLGIALDVAHLLHBTQPSMVHGDRVARNILLTAGFRAKLS	478
Query 455	NFSMAR--TFTNPMMSKIDVFAFGVVLIELLTGRKAMTTKENGEVVMILWKDIWKFQ-E	511
Sbjct 479	NFS+A+ + + DVFAFG++L+ELL+GR+A+ + E+ ML +I + D NFSLAKPAATVDAATSSDVFAFGLLLLELLSGRRAREARVGVEIGMLTEIRTVLADAG	538
Query 512	ENREERLKRWMDPKLDNYYPIDYALSLASLAVNCTADKSLSRPTIAIEIVLSSLTQP	569
Sbjct 539	+ R +LRKWMMPD L Y +D ALSLA +A CT + + RP +AEI SLS+L QP DKRAAKLKRWMDP TLGGEYGVDAALSLAGMARACTEEDAARRPKMAEIAFSLSVLGQP	596

>emb|CA002953.1| Lys-M-domain containing receptor-like kinase [Medicago truncatula var. truncatula]
Length=313

Score = 417 bits (1071), Expect = 3e-114, Method: Compositional matrix adjust.
Identities = 206/315 (65%), Positives = 252/315 (80%), Gaps = 3/315 (0%)

Query 53	YISQSPNFLSITSVSNIFDTSPLSIARASNQHQEEDKLIPIGQVLLIPVTCGCTGNRSFAN	112
Sbjct 1	Y+QSPNFLSLSNISDIFNLSPLRIAKASNIEAEDKKLIPDQLLVPVTCGCTKNHSFAN	60

Query 113 ISYEINQGDSFYFVATTLYQNLTNWAVMDLNPGLSQFTLPIGIQVVIPLFCKCPSKNQL 172
 I+Y I QGD+F+ ++ T YQNLTN+ + NP LS LP+ +V +PLFCKCPSKNQL 120
 Sbjct 61 ITYSIKQGDNFFILSITSYQNLNTYLEFKNFNPNLSPTLPLDTKVSPLFCCKCPSKNQL

Query 173 DRGIKYLITHWQPNDNVSFVSNKLGSAPQDILSENNYGCQNFATAASNLPVLIPTVLLPDL 232
 ++GIKYLIT+VWQ NDNV+ VS+K GAS ++I+ENN+ NFTA++N VLIPVT LP L
 Sbjct 121 NKGIKYLITYVWQDNDNVTLVSSKGASQVEMLAENNHH--NFTASTNRSVLIPVTSPLK

Query 233 IQSPSDGRKHRI-GLPVIIGISLGCTLLVVVSAILLVCVCCMKSLNRSAETADKL 291
 Q S+GRK L +IIGISLG ++V + LV V CLMK LNRS SS+ETADKL
 Sbjct 179 DQPSSNGRKSSSQNLALIIIGISLGSAFFILVLTSLVYVCLMKRILNRSTSSSETADKL

Query 292 LSGVSGYVSKPTMYETGAILEATMNLSEQCKIGESVYKANIEGKVLAVKRFKEDVTEELK 351
 LSGVSGYVSKPTMYE AI+E T NMLS+ CKIGESVYKANI+G+VLAVK+ K+D +EELK
 Sbjct 239 LSGVSGYVSKPTMYEIDAIMEGTMNLSDNCKIGESVYKANIDGRVLAVKKIKKDASEELK

Query 352 ILQKVNHNGLVKL 366
 Sbjct 299 ILQKVNHNGLVKL 313

>emb|CAO02964.1| LysM-domain containing receptor-like kinase [Medicago truncatula var. truncatula]
 emb|CAO02968.1| LysM-domain containing receptor-like kinase [Medicago truncatula var. truncatula]
 Length=311

Score = 414 bits (1065), Expect = 1e-113, Method: Compositional matrix adjust.
 Identities = 205/313 (65%), Positives = 251/313 (80%), Gaps = 3/313 (0%)

Query 53 YISQSPNFLSLSVSNIFDTSPSIARASNLLQHEEDKLIPIPGQVLLIPVTCGCTGNRSFAN 112
 Y+QSPNFLSL++S+IF+ SPL IA+ASN++ E+ KLIP Q+LL+PVTGCT N SFAN 60
 Sbjct 1 YRAQSPNFLSLSNISDIFNLSPRIAKASNIEADKKLIPDQIPLLVPVTCGCTKNHSFAN

Query 113 ISYEINQGDSFYFVATTLYQNLTNWAVMDLNPGLSQFTLPIGIQVVIPLFCKCPSKNQL 172
 I+Y I QGD+F+ ++ T YQNLTN+ + NP LS LP+ +V +PLFCKCPSKNQL 120
 Sbjct 61 ITYSIKQGDNFFILSITSYQNLNTYLEFKNFNPNLSPTLPLDTKVSPLFCCKCPSKNQL

Query 173 DRGIKYLITHWQPNDNVSFVSNKLGSAPQDILSENNYGCQNFATAASNLPVLIPTVLLPDL 232
 ++GIKYLIT+VWQ NDNV+ VS+K GAS ++I+ENN+ NFTA++N VLIPVT LP L
 Sbjct 121 NKGIKYLITYVWQDNDNVTLVSSKGASQVEMLAENNHH--NFTASTNRSVLIPVTSPLK

Query 233 IQSPSDGRKHRI-GLPVIIGISLGCTLLVVVSAILLVCVCCMKSLNRSAETADKL 291
 Q S+GRK L +IIGISLG ++V + LV V CLMK LNRS SS+ETADKL
 Sbjct 179 DQPSSNGRKSSSQNLALIIIGISLGSAFFILVLTSLVYVCLMKRILNRSTSSSETADKL

Query 292 LSGVSGYVSKPTMYETGAILEATMNLSEQCKIGESVYKANIEGKVLAVKRFKEDVTEELK 351
 LSGVSGYVSKPTMYE AI+E TMNLS+ CKIGESVYKANI+G+VLAVK+ K+D +EELK
 Sbjct 239 LSGVSGYVSKPTMYEIDAIMEGTMNLSDNCKIGESVYKANIDGRVLAVKKIKKDASEELK

Query 352 ILQKVNHNGLVKL 364
 Sbjct 299 ILQKVNHNGLVKL 311

>emb|CAO02944.1| LysM-domain containing receptor-like kinase [Medicago truncatula var. truncatula]
 Length=307

Score = 408 bits (1049), Expect = 1e-111, Method: Compositional matrix adjust.
 Identities = 201/309 (65%), Positives = 247/309 (79%), Gaps = 3/309 (0%)

Query 53 YISQSPNFLSLSVSNIFDTSPSIARASNLLQHEEDKLIPIPGQVLLIPVTCGCTGNRSFAN 112
 Y+QSPNFLSL++S+IF+ SPL IA+ASN++ E+ KLIP Q+LL+PVTGCT N SFAN 60
 Sbjct 1 YRAQSPNFLSLSNISDIFNLSPRIAKASNIEADKKLIPDQIPLLVPVTCGCTKNHSFAN

Query 113 ISYEINQGDSFYFVATTLYQNLTNWAVMDLNPGLSQFTLPIGIQVVIPLFCKCPSKNQL 172
 I+Y I QGD+F+ ++ T YQNLTN+ + NP LS LP+ +V +PLFCKCPSKNQL 120
 Sbjct 61 ITYSIKQGDNFFILSITSYQNLNTYLEFKNFNPNLSPTLPLDTKVSPLFCCKCPSKNQL

Query 173 DRGIKYLITHWQPNDNVSFVSNKLGSAPQDILSENNYGCQNFATAASNLPVLIPTVLLPDL 232
 ++GIKYLIT+VWQ NDNV+ VS+K GAS ++I+ENN+ NFTA++N VLIPVT LP L
 Sbjct 121 NKGIKYLITYVWQDNDNVTLVSSKGASQVEMLAENNHH--NFTASTNRSVLIPVTSPLK

Query 233 IQSPSDGRKHRI-GLPVIIGISLGCTLLVVVSAILLVCVCCMKSLNRSAETADKL 291
 Q S+GRK L +IIGISLG ++V + LV V CLMK LNRS SS+ETADKL
 Sbjct 179 DQPSSNGRKSSSQNLALIIIGISLGSAFFILVLTSLVYVCLMKRILNRSTSSSETADKL

Query 292 LSGVSGYVSKPTMYETGAILEATMNLSEQCKIGESVYKANIEGKVLAVKRFKEDVTEELK 351
 LSGVSGYVSKPTMYE AI+E TMNLS+ CKIGESVYKANI+G+VLAVK+ K+D +EELK
 Sbjct 239 LSGVSGYVSKPTMYEIDAIMEGTMNLSDNCKIGESVYKANIDGRVLAVKKIKKDASEELK

Query 352 ILQKVNHN 360
 Sbjct 299 ILQKVNHN 307

>emb|CAO02946.1| LysM-domain containing receptor-like kinase [Medicago truncatula var. truncatula]
 Length=305

Score = 404 bits (1037), Expect = 2e-110, Method: Compositional matrix adjust.
 Identities = 199/307 (64%), Positives = 245/307 (79%), Gaps = 3/307 (0%)

Query 53 YISQSPNFLSLSVSNIFDTSPSIARASNLLQHEEDKLIPIPGQVLLIPVTCGCTGNRSFAN 112
 Y+QSPNFLSL++S+IF+ SPL IA+ASN++ E+ KLIP Q+LL+PVTGCT N SFAN 60
 Sbjct 1 YRAQSPNFLSLSNISDIFNLSPRIAKASNIEADKKLIPDQIPLLVPVTCGCTKNHSFAN

Query 113 ISYEINQGDSFYFVATTLYQNLTNWAVMDLNPGLSQFTLPIGIQVVIPLFCKCPSKNQL 172
 I+Y I QGD+F+ ++ T YQNLTN+ + NP LS LP+ +V +PLFCKCPSKNQL 120
 Sbjct 61 ITYSIKQGDNFFILSITSYQNLNTYLEFKNFNPNLSPTLPLDTKVSPLFCCKCPSKNQL

Query 173 DRGIKYLITHWQPNDNVSFVSNKLGSAPQDILSENNYGCQNFATAASNLPVLIPTVLLPDL 232
 ++GIKYLIT+VWQ NDNV+ VS+K GAS ++I+ENN+ NFTA++N VLIPVT LP L
 Sbjct 121 NKGIKYLITYVWQDNDNVTLVSSKGASQVEMLAENNHH--NFTASTNRSVLIPVTSPLK

Query 233 IQSPSDGRKHRI-GLPVIIGISLGCTLLVVVSAILLVCVCCMKSLNRSAETADKL 291

Sbjct 179 Q S+GRK L +IIGISLG ++V + LV V CLKMK LNRS SS+ETADKL
 DQPSSNGRKSSQNLALIIGISAFFILVLTSLVYVYCLKMKRLNRSSTSSSETADKL 238

Query 292 LSGVSGYVSKPTMYETGAILEATMNLSEQCKIGESVYKANIEGKVLAJKRKFEDVTEELK 351
 LSGVSGYVSKPTMYE AI+E TMNLS+ CKIGESVYKANI+G+VLAJK+ K+D +EELK
 Sbjct 239 LSGVSGYVSKPTMYEIDAIMEGTMNLSDNCKIGESVYKANIDGRVLAVKKIKKDASEELK 298

Query 352 ILQKVNH 358
 ILQKVNH
 Sbjct 299 ILQKVNH 305

>emb|CAO02962.1| LysM-domain containing receptor-like kinase [Medicago truncatula]
 var. truncatula]
 Length=304

Score = 400 bits (1028), Expect = 3e-109, Method: Compositional matrix adjust.
 Identities = 198/306 (64%), Positives = 244/306 (79%), Gaps = 3/306 (0%)

Query 53 YISQSPNPLSLSLTSVSNIFDTSPLSIARASNLLQHEEDKLIPLGPQLLIPVTCGCTGNRSFAN 112
 Y+QSPNPLSLL++S+IF+ SPL IA+ASN++ E+ KLIP Q+LL+PVTGCT N SFAN
 Sbjct 1 YRAQSPNPLSLSNISDFNLSLSPRLIAKASNIEAEDKKLIPDQ111VLPVTCGCTKNHSFAN 60

Query 113 ISYEINQGDSFYFVATTLYQNLNTNWHAVMDLNPGLSQFTLPIGIQVVIPLFCCKPSKNQL 172
 I+Y I QGD+F+ ++ T YQNLNTN+ + NP LS LP+ +V +PLFCCKPSKNQL
 Sbjct 61 ITYSIKQGDNFFILSITSYQNLNTNLEFKNPNPLSPTLLPLDKVSVPLFCCKPSKNQL 120

Query 173 DRGIKYLITHWQPNNDNSVFSNKLQGASPQDILSENNYQGNFTAASNLPLVLIBVTLPLDL 232
 ++G+GKYLITH+VWQ+ NDNV+ VS+K GAS ++L+ENN+ NFTA++N VLIBVTL PL L
 Sbjct 121 NKGKYLITYVWQDNDNVTLVSSKFGASQVEMLAENNHH--NFTASTNRSVLIVFTSLPKL 178

Query 233 IQSPSDGRKHRI-CLPVIIGISLGCTLLVVVSAILLVCVCCLKMKSLSNRSASSAETADKL 291
 Q S+GRK L +IIGISLG ++V + LV V CLKMK LNRS SS+ETADKL
 Sbjct 179 DQPSSNGRKSSQNLALIIGISAFFILVLTSLVYVYCLKMKRLNRSSTSSSETADKL 238

Query 292 LSGVSGYVSKPTMYETGAILEATMNLSEQCKIGESVYKANIEGKVLAJKRKFEDVTEELK 351
 LSGVSGYVSKPTMYE AI+E TMNLS+ CKIGESVYKANI+G+VLAJK+ K+D +EELK
 Sbjct 239 LSGVSGYVSKPTMYEIDAIMEGTMNLSDNCKIGESVYKANIDGRVLAVKKIKKDASEELK 298

Query 352 ILQKVN 357
 ILQKVN
 Sbjct 299 ILQKVN 304

>ref|XP_002517029.1| Serine-threonine protein kinase, plant-type, putative [Ricinus communis]
 gb|EEF45192.1| Serine-threonine protein kinase, plant-type, putative [Ricinus communis]
 Length=615

GENE ID: 8280185 RCOM_0909430 | serine-threonine protein kinase, plant-type, putative [Ricinus communis]

Score = 356 bits (913), Expect = 6e-96, Method: Compositional matrix adjust.
 Identities = 221/584 (37%), Positives = 321/584 (54%), Gaps = 72/584 (12%)

Query 32 TNQTNFSCPSNSPPSCETYVTYISQSPNFLSLSLTSVSNIFDTSPLSIARASNLLQHEEDKLI 91
 T+G + S P C+T Y + +PNFL L SV ++F S L I+ SN+ LI
 Sbjct 30 TDGITCTVNTQTSNP-CQTYAFYRAMAPNFDLIALSAGDLSVSRIMISEPSNISSPSSPLI 88

Query 92 PGQVLLIPVTCG-----TGNRSFANISYEINQGDSFYFVATTLYQNLNTNWHAVMDLNPG 146
 P Q L +P+C C T N S+AN+SY I + D+F Y V+TT +QNLNT + AV +NP
 Sbjct 89 PNQSLFVPISCSCRAINSTTNSYANLSYTICKDDTFYLVSTTQFQNLTTYQAVQVNVPT 148

Query 147 LSQFTLPIG1QVW1PLFCKCPSQNQLDRGIKY1LITHWQPNNDNSVFSNKLQGASPQDILS 206
 L L IG ++V P+FCKCP++ QL + ++I++V+QP+DN+S V++ G + Q I+
 Sbjct 149 LVPTLLEIGQEVIFPVFCKCPNQTQLQNLQNVNFMSYVFQPSDNLSSLVASSFGNTNTQSIVD 208

Query 207 ENNYQCNFTAASNLPLVLPVTLPLDIQ-----SPSDGRKHRIGLPVIIGISLG-CTLLV 260
 N G N + +PV LP L Q S +K R GL + + LG C L+
 Sbjct 209 VN--GNNIQPFDT--IFVFPNRLPQLSQFVVVPSPVTEKKERKGLITGLAVGLGVCGFLL 264

Query 261 VVSAILLCVCCLKMKSLSNRSASS-----AETADKLLSGVSGYVSKPT 303
 IL++ + LNR S E KL++ VS + K
 Sbjct 265 ---ILIIGSWVFRGKLNRRKSEEDEDKKRLRFYKGEKGLTMETKLIADVSDCLDKYR 320

Query 304 MYETGALLEATMNLSEQCKIGESVYKANIEGKVLAJKRKFEDVTEELK1LQKVNHNGLVK 363
 +++ + EAT + E + SYK + I G+ A+K+ K + EELK1LQKVNHNGLVK
 Sbjct 321 VFKIDELATEDGFNENFLIQGSVYKGSINGQDYAIKKMKWNAYEELK1LQKVNHNGLVK 380

Query 364 LMGVSSDN-DGNCFVYVEYAENGSLLEWLFAKSCSETSNSRTSLTWCQRISIAVDVSMGL 422
 L G D+ DG+C++YEY ENGSL WL N L W R+ IA+DV+ GL
 Sbjct 381 LEGFCIDSEDGSCYLIYEIENGSLHSLWHLI-----NKNEKLNWKTRLRIAIDVANGL 433

Query 423 QYMHHEAYPRVHRDITSSNILLSDNSFKAKIANFSMARTFTNPM----- 467
 QY+HEH PR+VH+DI SSNILLDS +AKIANE +A++ N +
 Sbjct 434 QYIHEHTPRVHVHKDIKSSNILLSTMRAKIANFGLAKSGCNAITMHVGTQGYIAPEYL 493

Query 468 -----SKIDVFAGFVVLIELLTGRKAMTTKENGEVVLWFKD1WKIFD-QEENREERLRK 520
 +++DVF+FGVVL+EL++G++A+ E G V LW + +D EE + +RL+
 Sbjct 494 TDGVVSTRMDFVFSGVVLLELISGKEAI--DEEGRV--LWAKVSGNWGDNEEKKVKRLKG 549

Query 521 WMDPK-LDNYYPIDYALSLASLAVNCTADKSLSRPTIAEIVLSD 563
 +MD L ++ + + ++AV C RP++ +IV L
 Sbjct 550 FMDESLLRESCSMESIIHVMNVAVACLHKDPAKRPSMVDIVYLD 593

>ref|XP_002280070.1| PREDICTED: hypothetical protein [Vitis vinifera]
 Length=622

GENE ID: 100264758 LOC100264758 | hypothetical protein LOC100264758
 [Vitis vinifera]

Score = 348 bits (893), Expect = 1e-93, Method: Compositional matrix adjust.
 Identities = 214/590 (36%), Positives = 329/590 (55%), Gaps = 70/590 (11%)

Query 27 AQSQ-QTNGTNFSCPSN-SPPSCTETYVTYISQSPNFLSLTSVSNIFDTSPLSIARASN LQ 84
 Sbjct 27 +Q+Q + N T + C +N S C T+ Y + SPNFL L S+ ++F S L I+ SN+ 86
 SQAQPEPNATGYPPCSANLSSYPCHTFAYTATSPNFLDLASICDLFWVSRLMISEPSNIS
 Query 85 HEEDKLIPGQVLLIPVTCGC-----TGNRSFANISYEINQGDSFYFVATTLYQNL TNWHA 139
 + L+ GQ L +P+ C C T S+AN+SY I GD+FY V+T + NLT +++
 Sbjct 87 SPSNPLVAGQSLFVPLNCNSCNVNTTAISYANLSYTICKSGDTFYLVSTFSFLNLTYY S 146
 Query 140 VMDLNPGLSQFTLPIGIQVVIPLFKCKCPSKNQLDRGIKYLITHWQPNDNVSFVSNKLGA 199
 V +NP L L +G +V+ P+FCCKC++ QL G+ +LI+V+Q+P+DN++ V+ LG+
 Sbjct 147 VEIVNPTLVPTDLDVGDKVIFPIFCKCPNETQLRNGVNFLISYVFQPSDNLTGVAASLGS 206
 Query 200 SPQDILSENNYQGNFTAASNLPVLIPVTLPPDLIQ-----SPSDGRKHRIGLPVIIGI 252
 I+ N G N + +PV+ LP++ Q + S + R G VIIG+
 Sbjct 207 DTASIIDVN--GDNIQPQFQT--IFFPVPSRLPNISQPNVTASATSVRKVERKG--VIIGL 260
 Query 253 SLG---CTLLVV--VSAILLVCVCLMKMSL-----NRSASSAETADKLLSGVSGY 298
 ++G C +L+V + + V K+K + R L+ + VS
 Sbjct 261 AIGLGVCGLLVLILLIGVWVYRHVMVEKIKEIEGDKERPLVGRGTLKAEEVNLMADVSDC 320
 Query 299 VSKPTMYETGAAILETMNLSEQQCKIGESVYKANIEGKVLAVKRFKFEDVTEELKILQKVNH 358
 + K +Y + +AT SE+ I SVYK +I+G++ A+K+ K + EELKILQKVNH
 Sbjct 321 LDKYKVYGGIEELRDATAFGFSERSLIQGSVYKGSIDGELYAIKKMKWNAYEELKILQKVNH 380
 Query 359 GNLVKGMLGVSS-NDGNCFVVYEAENGSLLEWLFAKSCSETNSRTSLTWQCRI SIAVD 417
 GNLV+L G D D C++VYE+ ENGS+ WL + L W R+ IA+D
 Sbjct 381 GNLVRLEGFCIDPEDATCYLVFENGSLSQWLHG-----DRDEKLNWKNRRLIAID 433
 Query 418 VSMGLQYMHAEHAPRIVHARDITSSNILLDSNFKAKIANFSMARTFTNPMM----- 467
 V+ GLQY+HEH PR+VH+DI SSNILL N +AKIANF +A++ N +
 Sbjct 434 VANGLQYIHEHTRPRVHVHKDIKSSNILLDGNMRAKIANFGLAKSGCNAITMHIVGTQGYI 493
 Query 468 -----SKIDVFAFGVVLIELLTGRKAMTTKENGEVVMLWWDKIWKIFD--QEENR 514
 +++DVF+FGVVL+EL++G++A+ E G V LW I + E+ +
 Sbjct 494 APEYLAGDVVSTRMDVFSFGVVLLELISGKEAV--DEEGRV--LWMSARGILEGKDEKV K 549
 Query 515 EERLRKWMDPK-LDNYPIDYALSLASLAVNC TADKSLSRPTIAEVLSL 563
 +R++ WMD L +D +++ ++A CT RP++ +IV +L
 Sbjct 550 AKRVKDWMDGLLRESCSMDSVINVMAVATACTHRDPSKRPSMVDIVYAL 599

>emb|CBI26350.3| unnamed protein product [Vitis vinifera]
 Length=595

Score = 343 bits (881), Expect = 3e-92, Method: Compositional matrix adjust.
 Identities = 212/576 (36%), Positives = 324/576 (56%), Gaps = 69/576 (11%)

Query 27 AQSQ-QTNGTNFSCPSN-SPPSCTETYVTYISQSPNFLSLTSVSNIFDTSPLSIARASN LQ 84
 Sbjct 27 +Q+Q + N T + C +N S C T+ Y + SPNFL L S+ ++F S L I+ SN+ 86
 SQAQPEPNATGYPPCSANLSSYPCHTFAYTATSPNFLDLASICDLFWVSRLMISEPSNIS
 Query 85 HEEDKLIPGQVLLIPVTCGC-----TGNRSFANISYEINQGDSFYFVATTLYQNL TNWHA 139
 + L+ GQ L +P+ C C T S+AN+SY I GD+FY V+T + NLT +++
 Sbjct 87 SPSNPLVAGQSLFVPLNCNSCNVNTTAISYANLSYTICKSGDTFYLVSTFSFLNLTYY S 146
 Query 140 VMDLNPGLSQFTLPIGIQVVIPLFKCKCPSKNQLDRGIKYLITHWQPNDNVSFVSNKLGA 199
 V +NP L L +G +V+ P+FCCKC++ QL G+ +LI+V+Q+P+DN++ V+ LG+
 Sbjct 147 VEIVNPTLVPTDLDVGDKVIFPIFCKCPNETQLRNGVNFLISYVFQPSDNLTGVAASLGS 206
 Query 200 SPQDILSENNYQGNFTAASNLPVLIPVTLPPDLIQ-----SPSDGRKHRIGLPVIIGI 252
 I+ N G N + +PV+ LP++ Q + S + R G VIIG+
 Sbjct 207 DTASIIDVN--GDNIQPQFQT--IFFPVPSRLPNISQPNVTASATSVRKVERKG--VIIGL 260
 Query 253 SLGCTLLVVVSAILLVCVCLMKMSLNRASSAETADKLLSGVSGYVSKPTMYETGAILE 312
 ++G L L+ LK + +N L++ VS + K +Y + +
 Sbjct 261 AIG--LGGDKERPLVGRGTLKAEEVN-----LMADVS DCLDKYKVYGGIEELRD 307
 Query 313 ATMLNLSQCKIGESVYKANIEGKVLAVKRFKFEDVTEELKILQKVNHGNLVKLMGVSSD-N 371
 AT SE+ I SVYK +I+G++ A+K+ K + EELKILQKVNHGNLV+L G D
 Sbjct 308 ATGGFSERSLIQGSVYKG SIDGELYAIKKMKWNAYEELKILQKVNHGNLVRLLEGFCIDPE 367
 Query 372 DGNCFVVYEAENGSLLEWLFAKSCSETNSRTSLTWQCRI SIAVDVSMGLQYMHAEHAP 431
 D C++VYE+ ENGS+ WL + L W R+ IA+DV+ GLQY+HEH P
 Sbjct 368 DATCYLVYEFVENGSLSQWLHG-----DRDEKLNWKNRRLIAIDVANGLQYIHEHTRP 420
 Query 432 RIVHRDITSSNILLDSNFKAKIANFSMARTFTNPMM-----SKI 470
 R+VH+DI SSNILL N +AKIANF +A++ N +
 Sbjct 421 RVVHKDIKSSNILLDGNMRAKIANFGLAKSGCNAITMHIVGTQGYIAPEYLAGDVVSTRM 480
 Query 471 DVAFGVVLIELLTGRKAMTTKENGEVVMLWWDKIWKIFD--QEENREERLRKWMDPK-LD 527
 DV+FGVVL+EL++G++A+ E G V LW I + E+ + +R++ WMD L
 Sbjct 481 DVFSFGVVLLELISGKEAV--DEEGRV--LWMSARGILEGKDEKVAKRVKDWMDGLL R 536
 Query 528 NYYPIDYALSLASLAVNC TADKSLSRPTIAEVLSL 563
 +D +++ ++A CT RP++ +IV +L
 Sbjct 537 ESCSMDSVINVMAVATACTHRDP SKRPSMVDIVYAL 572

>gb|AAT00791.1| SYM10-like protein [Galega orientalis]
 Length=244

Score = 336 bits (862), Expect = 4e-90, Method: Compositional matrix adjust.
 Identities = 174/244 (71%), Positives = 200/244 (81%), Gaps = 3/244 (1%)

Query 222 VLIPVTLPPDLIQSPSDGRKHRIG-LPVIIGISLGCTLLVVVSAILLVCVCLMKMSLNR 280
 +LIPVTL P L Q S G LPVIIGISLG +VV + LV V CLMKM LNR
 Sbjct 1 ILIPVTNLPKLDQPSSSGSISSSSKLPLVIGISLGSAFFIVVLTSLVYYCLMKM LNR 60
 Query 281 SASSAETADKLLSGVSGYVSKPTMYETGAILEATMNLSEQQCKIGESVYKANIEGKVLAVK 340
 S AETADKLLSGVSGYVSKPTMYE I+EAT +LS+QCKIGESVYKANI+ + LAVK
 Sbjct 61 STSLAETADKLLSGVSGYVSKPTMYEIDVIMEATNDLSDQCKIGESVYKANIDSRLAVK 120
 Query 341 RFKEDVTEELKILQKVNHGNLVKLMGVSSDNDGNCFVVYEAENGSLLEWLFAKSCSETS 400
 + K+D +EELKILQKVNHGNLVKLMGVSSDNDGNCF+VYEYAENGSL++WLF++ S+TS
 Sbjct 121 KIKKDASEELKILQKVNHGNLVKLMGVSSDNDGNCFLVYEYAENGSLDDWLSEA-SKTS 179
 Query 401 NS-RTSLTWCQRI SIAVDVSMGLQYMHAEHAPRIVHARDITSSNILLDSNFKAKIANFSMA 459
 NS +SLTW QRI IA+DV+ +GLQYMHHEH YPRI+HR IT+SNIL+DSNFKAKIANF

Objct 180 NSIVSSLWSQRIGIAMDVAVGLQYMHEHTYPRIIHRYITTSNILIDSNFKAKIANFLDG 239

Query 460 RTFT 463

+T T

Objct 240 KTST 243

>**gb|ABR17803.1|** unknown [Picea sitchensis]
Length=536

Score = 333 bits (855), Expect = 3e-89, Method: Compositional matrix adjust.
Identities = 201/519 (38%), Positives = 282/519 (54%), Gaps = 65/519 (12%)

Query 107 NRSFANISYEINQGDSFYFVATTLYQNLNTNWHAVMDLNPGLSQFTLPIGIQVVIPLFCCKC 166
N S AN++Y I GD+FY ++T ++NLT + AV NP L L IG IP+ CKC
Sbjct 3 NYSQANVTYTIYGGDTFYLISTRKFENLTTYPAVEVTNPTLVVTNLQIGSLATIPIRCKC 62

Query 167 PSKNQLDRGIKYLITHVWQPNDNVSFVSNKLGASPQDILSENNYQGNFTAASNLPVLIPV 226
PS Q+ G K LI+T+V P D + +S K GA Q++ S N S L L+PV
Sbjct 63 PSNAQVTNTKMLITYVHVGDTLLNISQKFGADLQNLKSLINGINSTLIPYSTL--LVPV 120

Query 227 TLLPDLIQ-----SPSDGRKRHIGLPVIIGISLGCTLLVVSAILL 267
+ P L Q + S G H +IG S+G + VV A+L+
Sbjct 121 SQKPVLQAQPSSPPSPPPPPPLVVNNATSSGGHLHG---GAVIGASVGGSAAVCIALLI 177

Query 268 VCVCCLKMSLNRASS-----AETADKLLSGVSYVKPTMYETGAILEATMN 316
CV K +S +++ S +T KL++G+S V P MY + +AT N
Sbjct 178 FCVVIRKRRSYKQTTSISEDQRPPSDVGVKTKSMLMTGISDCVENPFMYSIEDLDKATQN 237

Query 317 LSEQCKIGESVYKANIEGKVLAVKRFKEDVTEELKILQKVNHGNLVKLMGVSSNDGNCF 376
S C I SVYK ++G+ A+K K D++ELKILQKVNH NLVKL GV ++G +
Sbjct 238 FSPLCNIEGSVYKGTLDGRDYAIKLMKGDISQELKILQKVNHNTLVKLEGVCISSEGQSY 297

Query 377 VVYEYAENGSLLEWLFAKSCSETSN----SRTSLTWQCRRISIAVDVSMGLQYMHEHAYPR 432
+VYEY EN SL WL E + S +SL W R+ +A+DV+ GLQY+HEH P
Sbjct 298 LVYEYIENSSLNTWLHDPEVENMSPIGWSSSLPWPKTRLQVALDVANGLQYIHEHTTPS 357

Query 433 IVHRDITSSNILLDSNFKAKIANFSMARTFTNPMMMS-----KID 471
+VH+DI SSNILLD NF+AKIANF MA++ N +
Sbjct 358 VVHKDIKSSNILLDGNFRKIANFGMAKSGINALTKHIMGTQGYMAPEYLADGFVSPKLD 417

Query 472 VFAGFVVLIELLTGRKAMTTKEN----GEVVMLWKDIWKFIDQEEENREERLRKWMDPKLD 527
VFAGFVVL+E++G+A+ + G+ +LW I + +E+ E +LRK+W+D L
Sbjct 418 VFAGFVVLLEMISGKEAIVRERGVPLAGKAGLWTQIRPLLEGED-IEGKLRLKWVDRNLLQ 476

Query 528 NYPPIDYALSLASLAVNCTADKSLSRPTIAEVLSL 566

Sbjct 477 NAYTMDISILGVATIARACVEEDPVARPTLPEIVYKLSNL 515

>**emb|CAN66762.1|** hypothetical protein [Vitis vinifera]
Length=591

Score = 328 bits (841), Expect = 1e-87, Method: Compositional matrix adjust.
Identities = 203/569 (35%), Positives = 312/569 (54%), Gaps = 59/569 (10%)

Query 27 AQSQ-QTNGTNFSCPSN-SPPSCETYVTVYISQSPNFLSLTSVSNIFDTSPLSIARASNQ 84
+Q+Q + N T + C + N S C T+ Y + SPNFL L S+ ++F S L I+ SN+
Sbjct 27 SQAQFEANATGYPCSANLSSYPCHTFAYTATSPNFLDLASIQLFWVSRLMISEPSNIS 86

Query 85 HEEDKLIPQVLLIPVTCGC-----TGNRSFANISYEINQGDSFYFVATTLYQNLNTNWA 139
+ L+ GQ L +P+ C C T S+AN++Y I GD+FY V+T + NLT ++
Sbjct 87 SPSNPLVAGQSLFVPLNCSCNSVNATTAISYANLTYTICKSGDTFYLVSTFSFLNLTTYS 146

Query 140 VMDLNPGLSQFTLPIGIQVVIPLFKCPSKNQLDRGIKYLITHVWQPNDNVSFVSNKLG 199
V +NP L L +G+V+P+FCKC++ QL G+ +LI+V+QP+DN++ V+ LG+
Sbjct 147 VEIVNPTLVPDTDLDVGDKVIFP+FCKCPNETQLRNGVNFLISYVFQPSDNLTQVAASLGS 206

Query 200 SPQDILSENNYQGNFTAASNLPVLIPVTLLPDLIQ-----SPSDG--RKHRIGLPVIIGI 252
I+ N G N + +PV+ LP++ Q SP+ R R G IIIG+
Sbjct 207 DTASIIDVN--GDNIQPFQT--IFVPPVSRLPNISQPNVTASPATSVRVERKG--AIIGL 260

Query 253 SLG---CTLLVV--VSAILLVCVCLMKSL-----NRSASSAETADKLLSGVSGY 298
S+G C +L+V + + V K+K + R + L++ VS
Sbjct 261 SIGLGVCGILLVLLIGVWVYRHVMVEKIKEIEGDKERPLVGRGSGLKAEEVNLADVSDC 320

Query 299 VSKPTMYETGAIIEATMNLSEQCKIGESVYKANIEGKVLAVKRFKEDVTEELKILQKVNH 358
+ K + Y + +AT SE+ I SVYK +I+G++ A+K+ K + EELKILQKVNH 380
Sbjct 321 LDKYKRVYGIELQGFSERSLIQGSVYKGSIDGELYAIKKMKWNAYEELKILQKVNH

Query 359 GNLVKLMGVSSD-NDGNCLVYVYEAENGSLLEWLFAKSCSETNSNRTSLTWQCRRISIAVD 417
GNLV+L G D D C++VYE+ ENGSL+ WL + L W R+ IA+D
Sbjct 381 GNLVRLEGFCIDPEDATCYLVYEVNGLSQSLWHLG-----DRDEKLNWKNRLRIAID 433

Query 418 VSMGLQYMHEHAYPRIHARDITSSNILLDSNFKAKIANFSMARTFTNPMMMSKIDVFAFGV 477
V+ GLQY+HEH PR+VH+DI SSNILLD NF+AKIANF +A++ N
Sbjct 434 VANGLQYIHEHTPRVVKHDKISSLNLLDGNMRKAKIANFGALKSGCN-----A 481

Query 478 VLIELLTGRKAMTTKENGEVVMLWKDIWKFID--QEENREERLRKWMDPK-LDNYYPIDY 534
+ + ++ + E G V LW I + E+ + +R++ WMD L +D
Sbjct 482 ITMHIVGTQGEAKADEEGRV--LWMSARGILEGKDEKVAKRVDWMDEGLLRESCSMDS 539

Query 535 ALSLASLAVNCTADKSLSRPTIAEVLSL 563

Sbjct 540 VINVMAVATACTHRDPSKRPSMVDIVYAL 568

>**ref|XP_001767824.1|** predicted protein [Physcomitrella patens subsp. patens]
gb|EDQ67338.1| predicted protein [Physcomitrella patens subsp. patens]
Length=658

Gene ID: 5931014 PHYPADRAFT_132645 | hypothetical protein
[Physcomitrella patens subsp. patens] (10 or fewer PubMed links)

Score = 309 bits (791), Expect = 8e-82, Method: Compositional matrix adjust.
Identities = 218/631 (34%), Positives = 328/631 (51%), Gaps = 98/631 (15%)

Query	25	IEAQSQQTNGTNFSCPSNSPPSCETYVTYI--SQSPNFLS LTSVSNI FDTSPLSIARAS	81
Sbjct	24	I SAQQQYRNTSGTCSGTT--RCQTYAFYRTAGSQS---TLTSIVLFN TSV EGIATAS	77
Query	82	NLQHEEDKLIP---GQVLLIPVTCGCTGNRSFANISYEINQGDSFYFVATTLYQNLTNWHD	138
Sbjct	78	++ + + + IP L IP+ C C N A S + I GD+ Y A Y Q LT W DV--DPNRTIPFNDRDPLIYIPLNCSFCNNTRALTSQIKSGDTMVKANGTYQGLTWE	135
Query	139	AVMDLNPGLSQFTLPIGQIYQVWFLPKCPSKNQDLRGKYLTHVWQPNNDNSFVSNKLG	198
Sbjct	136	A+ NP + + + G +VPI C CP+ Q G + L+T+ P+ + F+S AISVANPTVIITNMTVGDYLVIPLRCACPTTQRAGRSRILLTYSIFFDETLKFISGLFN	195
Query	199	ASPQDILSENNYQQNFTAAS-----NLPVLI PV TLL-----PDLIQSPSDGRKHRI GL	246
Sbjct	196	++ + NN + A+ LP L+P+E++ + P + + + P G + IPEVELQTANNGASSANLAFTTLLVPLPSLVLPLSTMKFPSPPPSVEAP--GPAPSTLV	253
Query	247	PVI-----IGISLGCTLLVVVSAILVCCVCLKMK-----LNR	280
PVI		IGI G + + A + L CV C +K	LNR
Sbjct	254	PVITNKDPSKTSMYI GIVFGFGMAL--AFILACVLCATVKRYKNIIRKIEYENRGLLNR	311
Query	281	SAS-----SAETAD- LILSGVSGYVS--KPTMYETGAILEATMNL SEQCKIGESVYKANI	332
Sbjct	312	+ S +TA+ L+SG+ K T + + AT + SE + I SV+ A + KSSVTIDSLDTANSSLVSGMTDLFGCDKLTKFSYEELDTATNHFSEDNRQISVFLAKI	371
Query	333	EGKVLA VFKEDVTEELKI LQKVNHGNL VKLMGV--SSDNDG--NCFVVYEAENGSL	388
Sbjct	372	G +A+KR K + + +E+K L +V+HGN+V+K L+G+ + D+DG N +VYEAENGSL NGSFVAIKPMKGNSMDELKILSLSQVHHGNVVKLVGMCARDSDGRSENLYIIVYEAENGSL	431
Query	389	EWLQCSSETNSNRS-----LTWCQRISIAVDVSMGLQYHMHEAYPRVHRDITTSNILL	445
Sbjct	432	+ L + TSN S L W R+ IAVD+ GL+Y+H + P +VH+D+ SSSNL DCLHHQMAYPTSNFSRSVGLLWNTRMQIAVDIASGLEYLHN YTNPSLVLHKDVKSSNILL	491
Query	446	DSNFKA KIANFSMARTFTN----PM-----SKIDVFAFGVVL	479
Sbjct	492	D NF+AK-ANF MA+ + P+M +K DVF+FGVVL DKNFRAKVANFGMAKPADSGEPGLMTEHIVGTQGYMAPEYLEHGLVSTKADVFSFGVVL	551
Query	480	I ELLTGRKAMTTKENGUVMLWKDIIWI KFDQQEENREERL R KWMDP KLDNYY PIDYIALS A +ELL+GR+A+ GE ML I + + + + L+ WMDP+L N YP D ALS+A	539
Sbjct	552	LELLSGREAI CNDGGGEFTMLSATISNVLSGDD-QMAK LQAWMDP RLQNAYPSDIALSVA	610
Query	540	SLAVNCTADKSLSRPTIAEIVL SLSLITQPS 570	
Sbjct	611	LA +C SRP + I +LS ++ S I LAKSCVETDPRSRPKDMQKISFALS KSMSSAS 641	

>[ref|XP_002311653.1|](#)  predicted protein [Populus trichocarpa]

gb|EEE89020.1|  predicted protein [Populus trichocarpa]

Length=524

GENE ID: 7473444 **POPTRDRAFT_564909** | hypothetical protein [Populus trichocarpa]
(10 or fewer PubMed links)

Score = 308 bits (788), Expect = 2e-81, Method: Compositional matrix adjust.
Identities = 180/500 (36%), Positives = 278/500 (55%), Gaps = 56/500 (11%)

Query	109	SFANISYEINQGDSFYFATTLYQNLTNWHAWMDLNPGLSQFTLPIG1QVW1PLFCKCPSS ANI+Y I +G+FV V+T +QNLN + +V NP L L IG++V+ P+FCKCP	168
Sbjct	13	SSANITYTIEAGNTFYIVSTKFQNYQLTYYQSVELNFNPTLLEPPILEDIGVEVIFPIFCKCP	72
Query	169	KNQLDRGIKYLITHWQPNDNVSFVSNKLGASPQDILSENN----YQQNFTAASNLFPVL +_QL + _YL++V+PQ+DN+S V++ G Q I+ N Y F + LP L QTQLQNKVNLYLSVYFQPSDNLSVASTFGVETQSIVDVNGNNIQPYDTIFVFPVNQLPQL	223
Sbjct	73	QTQLQNKVNLYLSVYFQPSDNLSVASTFGVETQSIVDVNGNNIQPYDTIFVFPVNQLPQL	132
Query	224	I-PVTLLPDLIQLQSPSDGRKHRIGLPLVIQGIGLSLGCCTLWVVAISALLVCVCCLLMK----- P ++P P + + + + +G+ + LLV-VS + LK +	276
Sbjct	133	AQPTVVVPSPGAPPPEKTERKGVIIGLAVGLGIAGLLLVLVSGVWFYREGVLIKRRDVEKV	192
Query	277	-----SINRSASSAETAD-KLLSGVGSGVSKPTMYETGAILETAMNLNSEOCKIGESVYK LN + + + + L++ VS + K +++ + EAT SE C I SV+K	329
Sbjct	193	EEKRRMQLNGGSKGLKDIEVSLMADVSDCLDKYRVRFKIDELKEATNGFSENCLIEGSVFK	252
Query	330	ANIEGKVLAVKRFKFEDVTEELKILQKVNHGNVLKLMGVSSD-NDGNCFVVYEEAENGSL +I G+ A+K+ K + EELKILQKVNHGNVLK G D D NC++VYE++G+GSL	388
Sbjct	253	GSIINGETYAIKKMKWNACEELKILQKVNHGNVLKLEGFCIDPEDANCYLVYEFVDSGSLH	312
Query	389	EWLFAKSCSETNSRTSLITWCORISIAVDSVMSGLQYMHAYEHPRIVHRDITSSNILLDSN WL N + +L+W+ R+ +A+DV+ GLQY+HEH PR+V+H+DI SSNILLDSN	448
Sbjct	313	SWLH-----RNEKEKLSWKTRLRVAIDVANGLQYIHEHTRPRVVFHKDIKSSNILLDS	365
Query	449	FKAKIANFSMARTFTNPM-----SKIDVFAFGVVLIELLTTGRK +AKIANF +A+T N + + +DV+FGVVL+EL+GR+GR+	487
Sbjct	366	MRAKIANFLAKTCNCNAITMHIVGTQGYIAPEYLAGDGVVSTRMDVFSFGVVLLELISGR	425
Query	488	AMTTKENGEVVMLWKDIWKFID---QEENREERLRKWMDPK-LDNYYPIDYALSLASLAV A+ E G+V LW + + + +E + +RL WMD L+ ++ ++ ++A+	543
Sbjct	426	AI---DEEGKV--IWAEAIGVLEGNVEERRKVKRLTAWMDKVLLEESCSMESVMNTMAV	481
Query	544	NCTADKSLSRPTIAEIWLSS 563	
Sbjct	482	ACLRHDPSKRPSMVDIVYAL 501	

>gb|EAY87082.1| hypothetical protein OsI_08480 [Oryza sativa Indica Group]
Length=651

Score =	299 bits (765),	Expect =	8e-79,	Method:	Compositional matrix adjust.
Identities =	196/601 (32%),	Positives =	307/601 (51%),	Gaps =	85/601 (14%)
Query 36	NFSPNSNPPSETYVTYISQSPNF-LSLTSVSNIFDSTSPLSIARASNLQHEEDKLIPGQ	94			
	F+C +N+ C Y + L ++ ++F S +A A+NL L Q				
Sbjct 39	GFnCTANATYPCPAVALYRAGFGGVPLEFAAIGDLFAASRFMVHAHNLSTSA-VLAARQ	97			
Query 95	VLLIPVTPCGCTGN--RSFANISYEINQGDSFYFATTLYQNLTNWHAVMDLNPGLSQFTL	152			
	LL+P CGC +A+ +Y+IN GD+++ V+TT QNLT + AV +NP L L				
Sbjct 98	PLLVLPLQCGCPSRSPNAYAPMQYQINAGDTYWIVSTTKLQNLTQYQAVERVNPTLVPTNL	157			
Query 153	PIGIQVVIPLFKCPSKNQLDRGIKYLITHVWQPNDNSVFSVSNKLQGASPQDILSENNYQQ	212			

>emb|CA002950.1| LysM-domain containing receptor-like kinase [Medicago truncatula]
var. truncatula]
Length=243

Score =	298 bits (762),	Expect =	2e-78,	Method:	Compositional matrix adjust.
Identities =	150/245 (61%),	Positives =	189/245 (77%),	Gaps =	3/245 (1%)
Query 53	YISQSPNPLSLSLTSVSNIFDTSPLSIARASNQLHEEDKLIPGQVLLIPVTCGCTGNRSFAN				112
Sbjct 1	Y+QSPNPLSLSL++S+IF+ SPL IA+ASN++ E+ KLIP Q+LL+FVTCGCT N SFAN				60
Query 113	ISYEINQGDSFYFVATTLYQNLTNWHAHMDLDNPGLSQFTLPIGIQVVIPLFKCPSKNQL				172
Sbjct 61	I+Y I QGD+F ++ T YQNLTN+ + NP LS LP+ +V +PLEFKCPSKNQL				120
Query 173	DRGIKYLITHWVQPNDNVSFVSNKLGASPDILSENNYQGNFTAASNLPVLIPVTLPLDL				232
Sbjct 121	++GIKYLIT+VWQ NDNV+ VS+K GAS ++L+ENN+ NFTA+N VLIPTV LP L				178
Query 233	IQSPPSDGRKHRI - GLPVIIGISLGC TLVVVSAILLCVCKMKSLLNRSAASSETADKL				291
Sbjct 179	Q S+GRK L +IIGISL + +V + LV C LKMK LNRS SS+ETADKL				238
Query 292	LSGV S 296				
Sbjct 239	LSGV S 243				

>dbj|BAI79278.1| LysM type receptor kinase [Lotus japonicus]
Length=666

Score = 293 bits (750),	Expect = 5e-77,	Method: Compositional matrix adjust.
Identities = 192/636 (30%),	Positives = 328/636 (51%),	Gaps = 99/636 (15%)
Query 14	I LYVVLMMFFTCI---EAQSQQTNGTNFSCPS-----NSPPSCETYVTYISQSPN +L V+++ F+ +AQ + N C + NS SC++Y+T+S SP	59
Sbjct 18	LLLVMVIISFSHMPISTQAQQEYVNNKQLDCDTQYNTTYGNVCNSVTSCSQSYLTFKSSPE	77
Query 60	F LSLTSVSNIFDTSPLSIARASNLQHEEDKLIPGQVLLIPVTCGCTGNRSFANISYEINQ ++ + S+S + +++P +A+++N+ + I ++ +PTVC C+G R N +Y + +	119
Sbjct 78	YNTPSSYLLNSTPSSLVAKSNNIT-DVTPIIYTDTMVTVPVTCSCSGGRYQHNATLYNKK	136
Query 120	-GDSFYFVATTLYQNLNTWHAVMDLNPGLQSQTLPGLIQVVIPLCPKSQNLDRLGIY G+++ +A YQ+LT A+M NP ++ L G + +PL C CP+K Q D G KY	178
Sbjct 137	TGETYFSIANNTYQSLTTCQALMAQNPyDAK-NLFAGDDLHVPLRCACPTKKQSDAGFKY	195
Query 179	LITHWQPNNDNVSFVNKLGASPQDILOSENNYQGNFTAASNLPVLI+F-TLLPDLIQ-- L+T++ ++ ++ G Q +L N P+T+ T P +Q	234
Sbjct 196	LLTLYLVSQGESPDSDIAEIFGVDTQSVSLDANEELDSKSVVFYFTPLVPLKTEPPARLQIAA	255
Query 235	-----SPSDGRKRHRIGLPIIIGISLGCTLLVVVSAI1LLVCVCL----- S S +K VI+G++G + +VV+ LLV C	273
Sbjct 256	SPPESPPPPAPAGNDSSSSKKW-----VIVGVTVGVAVCLVVA--LLVFLFCYNRRQQ	308
Query 274	-----KMKSINRSASSAAETAKDLLSGVSGGYVSKPMTYETGAILEATMLNSE +K ++ + + E+ GV + T Y+ G I AT SE	319
Sbjct 309	PAPPVSVKDFPDSAVKMVSETPTTESWSLSSEGVRAYAIESLTAYKFQDIQATKFFSE	368
Query 320	QCKIGESVYKANIEGKVLAVKRFKEDVTEELKILQKVNHGHLVQLMGVSSDNGNCFVVY + KI SVY+A+ G AVK DV+ E+ +L+++NH N++L G + GN +VY	379
Sbjct 369	ENKIKGSGSYRASFKGDDAAVKILNGDVSAEINLLKRINHANIIRLSLGFVC-HKGNTLYVY	427
Query 380	EYAENGSSLEEWLFRAKSCSETSNSRTSLWTQCRIASIAVDVSMGLQYMHHEHYPRIVHRDIT E+AAN SL++WL + + S SL+W QR+ IA DV+ L Y+H + P +H+++	439
Sbjct 428	EFAENDSLDDWLHSDKKYQNS--VSLSWMQRVQIAYDVADALNLHNYTNPIIHKNLK	484
Query 440	SSNILLDSNFKAKIANFSMARTFTNP-----MMSKID	471
Sbjct 485	SGNVLLDGKFRAKVSFNGLARVMEDQGEDGGFQMTRHVVGTQGYMPPEYIESGLITPKMD	544
Query 472	VFAFGVVLIELLRTKRMATTKEN--GEVVMLWKDIWKFIDQEENREERLRKWMDPKLDN VFAFGV++ELL+GR+A ++ E GE ML + + + +N ++LB +MDP L +	528

Sbjct	545	VFAFGVVMLELLSGREATSSGEKNGLGENKMLSETVNHL-EGDNVRDQLRGFMDPTLRD	603
Query	529	YYPIDAYALSLASLASLAVNCTADKSLSRPTIAEIVLSSL Y+P+D A S+A +A C A SRP I+E+++LLS	564
Sbjct	604	EYPLDLAYSMAEIAKRCVAHDLNSRPNISEVIMTLS	639

>ref|XP_001783589.1| predicted protein [Physcomitrella patens subsp. patens]
>gb|EDG51621.1| predicted protein [Physcomitrella patens subsp. patens]
Length=637

GENE ID: 5946784 PHYPADRAFT_152558 | hypothetical protein
[*Physcomitrella patens* subsp. *patens*] (10 or fewer PubMed links)

Score = 285 bits (729), Expect = 1e-74, Method: Compositional matrix adjustment
Identities = 193/614 (31%), Positives = 310/614 (50%), Gaps = 77/614 (12%)

Query	27	AQSQQTNTGNTFSCPSNSPPS--CETYVTYIISQSPNFLSLSLTSVSNIFDTSPLSIARAS--	81
Sbjct	2	AQ+ + C N+ PS C T+ Y+ SL V+ F+ + ++A S AQQNYYNDTEGYAC--NAAPSSTSCSTFYARTFQAG=ESLRKVNGRNKTAANAVANVSHAWM	58
Query	82	NLQHEEDKLIPGVQLLIPVTCGCTGNRSFANISYEINQDSFSYFVATTLYQNLTNWHAWM	141
Sbjct	59	NL L Q L +P+ C C RS +S+ I +GD+F+ ++ T Y LT + A+M NLLSTTASLKQTQALYVPLDCRCLNARSQMQVSHTIVRGDTFWLLSVTEYGGLTRYQAMM	118
Query	142	DLNPGLSQFTLPiGIVQV1PLKCPKCSQNLDGRIGKYLITHWQPNDNVSFVNKNLKGASP	201
Sbjct	119	NP + L IG + +P+FC CP+ Q+ G YL+T P++ + +S + G S ASNPSKDVNNLTGDTITVPIFCAPCTAAQVANGTNLVNTTTVYPSETLDIISARFGIST	178
Query	202	QDILSENNYQGNFTAASNLPVLIPIVTLPLD-----IQSPSDG--	239
Sbjct	179	D+ NN + N +L+P+ LP L + SP+ TDLSRANNVNSSILDVNTTLLVPLATLPPATMDWAPVTSQPPPSPATVASPNAAPAV	238
Query	240	-RKHRIGLPLVIIGISLGCTLVVVSAILLWVCLVKCMLKMSLNRSASSAETADK-----L	291
Sbjct	239	K P+ IGI+G L + + L+ + S + E + L ITKSASQTPLYIGIAVGAFGLTAAVFALLLKFASRNNSGTKPKDLMTEEMKRPNMVHTEL	298
Query	292	LSGVSGYVS--KPTMYETGAILEATMNLSSEQCKIGESVYKANIEGKVLAVKRFKEDVTEE	349
Sbjct	299	L+G+S V KP + I AT S + I SVYK I G++A+K+ K ++T+E LAGMSDMVGSEKPVULLSHEEIQSATQGFSENPIGGSVYKGCINGQLVAIKQMGNMHQE	358
Query	350	LKILQKVNHGVLKVLGMVSSDNDGNCFVVEYYEAENGSLLEEWLFAKSC---SETSNSRTS	406
Sbjct	359	LKIL +V+H NLVKL+G+ N ++VYEYA++GSL + L + + + S S L LKILCQVHHSNLVKGVLCVGGSENLYLVYEAHKGSLNDCLRNQAIIGRITFTSQSAAYL	418
Query	407	TWCQRISIAVDWSMGLQYMHAEHYAPIVRHDITSSNLLDSNFSKAKIANFSMARTFTN--	464
Sbjct	419	WC R+ I+DV+ GL+Y+H + P VH+D+ +SNIILD NF+AK+ANF MA++ + PWCSRVRIALDVASGLEIYHNTPSFVHDKVDTNSNLLDENFRAKVANFGMAKSAAASAD	478
Query	465	--PMMS-----KIDVFAFGVVLIELLTGRKAMTTKENGEVVML	500
Sbjct	479	P+++ K DV+AFGVV+E+L+G++A+ E E AGPLLTRHITGTQGYMAPEYLEHGLVTVKADYVAFGVVLELPSLKGAEAVRPRKEDEEQG	538
Query	501	WKD-----IWKIFDQ--EENREERLRKWMDPKLNDNYYPIDYALSLASLAVNCADKSL	552
Sbjct	539	K+ I + + E + E+L+R+D+P+L + YPI+ A S+ASLA+ C VKERALSDIIVDVLNAGTAEQLRKFIDPQLHSAYPIEIASIASSLASLAMTCIDPDPAV	598
Query	553	RPTIAEIVLSSL 566	
Sbjct	599	RPP++ ++LS + RPSMKDVTFLASKM 612	

>[ref|XP_002326901.1|](#) predicted protein [Populus trichocarpa]
>[gb|EEE73651.1|](#) predicted protein [Populus trichocarpa]
Length=609

GENE ID: 7470467 POPTRDRAFT_591844 | hypothetical protein [Populus trichocarpa]
(10 or fewer PubMed links)

Score =	285 bits (728),	Expect = 1e-74,	Method: Compositional matrix adjust
Identities =	185/556 (33%),	Positives = 295/556 (53%),	Gaps = 54/556 (9%)
Query 46	SCETVYISQOSPFLSLSLTSVNSNIFDTSPLSIARASNLQHEEDKLIPGQVLLIPVTCGCT	105	
Sbjct 54	SCQAFLIFKFSQ-PSFNSVPSISALTSANQEELARINNVTRLSEFPNNVEI-VPVNCFC	111	
Query 106	GNRFSFANISYEINQG-DSFYFVATTILYQNLNTNWHAVMDLNPLGLSQFTLPIGIVQVVIPLFC	164	
Sbjct 112	G AN ++ +Y+A Y+ L+ A+ LN ++ L G ++ +PL C GQYYQANTTIQVTTTRGTYYVIANETYEGLSTAALKHLNIH-GEYDLLPGEELQVPLRC	170	
Query 165	KCPSKNQLDRGIKYLITHVWQPNNDNSVFSNKLGASPQDILNENNYGQNFTAASNLPVLI	224	
Sbjct 171	CP+ NQ+ RG KYL+T+ +DN+ +++ S +DIL N +N T + +LI ACPTTNQMIRGTYKLVTVPLSSDDNPIFDIADRKFVSTKDILDANGMEENPTLYPDTTILI	230	
Query 225	PVTLPLDPLIQS-----PS-----DGRKRHIGLPIVIGISLGCTLLVVSAIILVCV	270	
Sbjct 231	P+ P Q+ PS R+ G++ C+LLV+ +V+ PLPTQSTSQTIIHSNPNISPPSALSPPRNRSKKHHYESGALAAACSSLVISIITAVVFL	290	
Query 271	CCLKMK---SLNRASSAETADKL1LSGVSGYVSKPTMYETGAILEATMNLSEQCKIGS	326	
Sbjct 291	C K + R A D+ ++ Y +++ + +AT NLS + +I S SCKKTREKVSGRGRERKQAVPED-IRVEIASYEQVLKVFKFEEVRKATENLSSSERINGS	349	
Query 327	VYKANIEGKVLAVKRFKEDVTEELKILQKVNHGNGNLVKGMLGVSSNDNGNCVVEYYAENG	386	
Sbjct 350	VY+ G++ LAK+ DVT+E+ IL++NH NL+KL GV +N G + +V EY ENGS VYRGEGFGEEILAVKMSRDVTKEVNI1LKRNHFNN1LEGCV-ENRGCFYLVLEMNGS	408	
Query 387	LEEWLFAKSCSETNSRSTSLLTWCQRISIAVDVSMGLQYMHEAYPRIVRHDITSSNILL	446	
Sbjct 409	L EWL K ET N W QRI IA+DV+ GL Y+H P VH+DI SSN+LL+ LREWLSCKKFEETGN-----WAQRQIALDVANGLYLHSFTEPAYVHKDIKSSNVLLN	462	
Query 447	SNFKAKIANFSMARTFTNPMM-----KIDVFAFGVVLIELLT	484	
Sbjct 463	N+AKIANFS+AR T+ M+ KIDV+AFGV+L+L+T GNLRAKIANFSLARAATSAAMTKHVGSIGYMAPEVYREGQVTPKIDVYAFGVILLEIT	522	
Query 485	GRKAMTTKENGEVVMILWKDIWIKFQDEENREERLRKWMDPKLDNYYPIDYALSLASLAVN	544	

Sbjct	523	G+ A+ T ++G +L +I+ I + +N E L ++DP L + +AL LA ++V GKDADVFT-QDGREALSTEIFSIMEN-KNPEVELDFVDPALKGSCGTNFALCLAKVSVA	580
Query	545	CTADKSLSRPTIAEIV 560 C + RP++ E+V	
Sbjct	581	CLMKEPARRPSMEEVV 596	

>ref|XP_002510756.1| kinase, putative [Ricinus communis]
gb|IEF52943.1| kinase, putative [Ricinus communis]
Length=634

Gene ID: 8269969 RCOM_1602540 | kinase, putative [Ricinus communis]

Score = 284 bits (727), Expect = 2e-74, Method: Compositional matrix adjust.
Identities = 188/575 (32%), Positives = 291/575 (50%), Gaps = 80/575 (13%)

Query	46	SCETYYTISQSNSLTSVNS---DTSPLSIARASNLQHEEDKLIPGQVLLIPVTC 102 SC++Y+T+ S P + + +S +F D++ L IA +N+ + + P L IPV C
Sbjct	56	SCQSYLTFRSAPPYTTPTVTSYSLQDSASI-IASLNNISSDVSSIPPQSQFLIPVNC 114
Query	103	GCTGNRSFA-NISYEINQGDSFYF-VATTLYQNLTNWHAVMMDLNPGLSQFTLPIGIQVVI 160 C G + + N SY + YE VA YQ L+ A+M NP L +G+++ +
Sbjct	115	SCFGQQFYQHNASYTLKFSSETYFSVANNDTYQGLSTCQALMSQNP-YGDRNLSVGMRLOV 173
Query	161	PLFKCKPSKNQLDRLGIKYLITHWQPNNDNVSVFVSNKLKGASPQDILSENNYQGNFTAASNL 220 PL C CP+ NQ G +YL+T++ D +S ++ G PQ IL N
Sbjct	174	PLRCACPTSNQTALGFYRLTYMVWGDITISSIAELFGVRPQSIILDANQLSSTSIIIFPFT 233
Query	221	PVLLPVTLPLDLIQS-----PSDGRKRIGLPIVIGISLGCTLLV--V 262 P+L+P+T P I++ PS G + +G+ LG LL++ V
Sbjct	234	PILVPLTTPPTTICASPPPPVSPPPPPLTPVLPSSGGSSRKW---TYVGVLGAALLLIFAV 290
Query	263	SAIIL-----VCVCKLKMDSL--NRSASSAETADKLLSGVGSGVSKPTMYETGAIL 311 S L + + K+L + SA ++ G + T+Y+ +
Sbjct	291	SGFLFWYPKSRSRKLTTVPIPSSALQSDSSAVPPDSSTPWRSRSAYGVIESLTLYKFHDLO 350
Query	312	EATMNLSEQCKIGESVYKANIEGKVLAVKRFKEDVTEELKILQKVNHGNLVKLMGVSSDN 371 AT SE+ +I SYVK + +G AVK K DV+ E+ IL+K+NH N+++L GV
Sbjct	351	LATDYFSEKNRIKGSVYKGSFKGDAAAVKVMKGDSSEISILKKINHSNIIRLSGVCL-Y 409
Query	372	DGNCFVYVEYAENGSLLEEWLFAKSCSETNSNRTSLTWCQRISIAVDVSMGLQYMHEHAYP 431 D N ++VYE+AENGSL E N +LTW QR+ IA DV+ L Y+H + P
Sbjct	410	DANTYLVFEAENGSLAE-----NVQT-LTWKQRVQTAHDVADALNYLHNNTNP 457
Query	432	RIVHRDITSSNILLDSNFKAKIANFSMARTFTNP----- 465 +H+++ +SNIILD+N +AKIANF +ART N
Sbjct	458	PYIHKNLKTSNILLDANMRAKIANFGIARTLQNNEAEGGLHLTRHVVTQGYMAPEYMENG 517
Query	466	-MMSKIDVFAFGVVLIENLLGRAMTTKENGEVVMLWKDIWKFIDQEEENREERLRKWMDP 524 + K+DVFAGVV+ELL+G+A T +N ML I ++ + +N +L +MDP
Sbjct	518	VITPKLDFVAFGVVILELLSGKEATAFYDKNAREEMLSASICRVL-EGDNVRHKLCGFMDP 576
Query	525	KLDNNYPIDYALSLASLASLAVNCTADKSLSRPTIAEI 559 L YP+D A SLA LA C + +RP+++++
Sbjct	577	SLGKQYPLDLAFSLAQLAQTCISHDINARPSVSQV 611

>**dbj|BAI79277.1| LysM type receptor kinase [Lotus japonicus]**
dbj|BAI79287.1| LysM type receptor kinase [Lotus japonicus]
Length=667

Score = 283 bits (724), Expect = 5e-74, Method: Compositional matrix adjust.
Identities = 193/663 (29%), Positives = 339/663 (51%), Gaps = 104/663 (15%)

Query	18	VLMFFTCIEAQSOQ-----TNGTNFSCPSNSPPSCETYVTYISQSNSFLSTS 65 + F E Q+QQ T+ + + NS SC++Y+T+ S SP + + +S
Sbjct	21	AMSFHMISETQAQOEYLNNSNQLCDNTHNSTYGNVNCNSVTSCQSYLTFKSSSPEYNTFSS 80
Query	66	VSNIFDTSPLSIARASNLQHEEDLIPQVLLIPVTCGCTGNRSFANISYEINQ-GDSFY 124 +S + + +P +A++N+ + +I + + +PVT C +G R - N +Y + + G++++
Sbjct	81	ISYLLNSTPSLVAKSNNIT-DVTPIITDTMVTVPVTCSCSGGRYQHNAATYNLKKTGETYF 139
Query	125	FVATTLQNLTNWHAVMIDLNPGLSQFTLPIGQVVIPLFCKPSKNQLDRLGIYKYLITHW 184 +A YQ-LT A+M NP ++ L G + +PL C CP+K Q D G KYL+T++
Sbjct	140	SIANNTYQSLSTTCQALMAQNPYDAK-NLFAGDDLHVPLRCAPTKKQSDAGFKYLLTYLV 198
Query	185	QPNDNVSVFVSNKLKGASPQDILSENNYQGNFTAASNLPVLI+PV-TLLPDLIQ----- 234 ++ + + G Q +L N P+L+P+ T P +Q
Sbjct	199	SQGESPDSDIAEIFGVDTQSVDANELESKSVVVFTPLVPLKTEPPARLQIAASPPESP 258
Query	235	-----SPSDGRKRIGLPIVIGISLGCTLLVVSAILLVCVCL----- 273 S S +K VI+G++G + +VV+ LLV C
Sbjct	259	PPAPAGNDSSSSKKW---VTVGVTGVAVCLVVA--LLVFLCFYNRRRRQPAPPPV 311
Query	274	-----KMKSLNRSSAETADKLLSGVGSGVSKPTMYETGAILEATMNLSEQCKIGE 325 +K ++ + + E+ GV + T Y+ G I AT SE+ KI
Sbjct	312	SVKDFPDSSAVKMSSETPTTESWSLSSSEGVRVIAIESLTAYKFGDIQQTATKFFSEENKIKG 371
Query	326	SVYKANIEGKVLAVKRFKEDVTEELKILQKVNHGNLVKLMGVSSDNDGNCFVYVEYAENG 385 SVY+A+ +G AVK DV+ E+ +L++N+ NH N++L G + CN ++VYE+AEN
Sbjct	372	SVYRASFKGDDAAVKILNGDVSAAEINLLKRINHANIIRLSGFCV-HKGNTYLVYFAEND 430
Query	386	SLEELWFAKSCSETNSNRTSLTWCQRISIAVDVSMGLQYMHEHAYPRIVHRDITSSNILL 445 SL++WL ++ + S SL+W QR+ IA DV+ L Y+H + P ++H++ S N+LL
Sbjct	431	SLDDWLHSEKKYQNS---VSLSWMQRVQIAYDVADALNYLHNNTNPVLIHKNLKSGNVLL 487
Query	446	DSNFKA KIANFSMARTFTNP-----MMSKIDVFAFG 476 + F+AK++NF +AR + + K+DV+AFG
Sbjct	488	NGKFRAKVSNGFLGALARAMEDDQGEDGGGFQMTRHVVGQTQGYMPPEYTENGLITPKMDVYAFG 547
Query	477	VVLLIELTGRKAMTTKEN---GEVVMLWKDIWKFIDQE-ENREERLRKWMDPKLDNYYPI 532 VV++ELL+G++A + GE +L + + + +N ++LR +MD L + YP+
Sbjct	548	VVMLELLSGKEATGNGDKNLGEKMLVLSSETVNHVLEGDNDNVRDKLRGFMQDQTLRDEYPL 607
Query	533	DYALSLASLAVNCTADKSLSRPTIAEI VLSLSLLQPSPATLERSLTSSGLDVEATQIVT 592 D A S+A +A C A SRP I+E+ ++LS + +TL+ +S +VE ++ V+

Subject 608 DLAYSMAEIAKRCVAHDLNSRPNISEVFMTLS---KVQSSTLDWPSS---EVERSRVS 661
 Query 593 SIS 595
 Subject 662 QIS 664

>emb|CBI17583.3| unnamed protein product [Vitis vinifera]
 Length=1305

Sort alignments for this subject sequence by:
 E value Score Percent identity
 Query start position Subject start position
 Score = 277 bits (708), Expect = 3e-72, Method: Compositional matrix adjust.
 Identities = 182/594 (30%), Positives = 305/594 (51%), Gaps = 70/594 (11%)
 Query 16 YYVLMFFTCIEAQSQQTNGTNFSCPSNSPPSCTYVTVYISQSPNFLSLTSVSNSNIFDTSPL 75
 Y + + +TC NG N + + +TY+ + S+SP + + +S+S++ + P
 Subject 705 YTTVGLYTC-----NGVN-----TTCQTYLIFRSESVYNNVSSISDLLASDPS 747
 Query 76 SIARASNLQHEEDKLIPGQVLILIPTCGCTGNRSFANISYEINQGDSFYFVATTLYQNLT 135
 +A+ + +E + + +PV C C+GN S N SY + GD + +A +Q L+
 Subject 748 QLAQINSVT-ETATFDNTKEVIVPVCNSCSGNYSQNTSYVVKNGDYPLWIANNTFQGLS 806
 NWHAVMDLNPGLSQFTLPIGIQVVIPLFCKCPSKNQLDRGIKYLITHVWQPNDNVFSVSN 195
 A++ NP +S L G + +PL C C+P+K Q D G+Y+L++++ D VS +S
 Subject 807 TCQALLNQNPNPSVATNLNPGBTVPLRCACPTKAQSDAGVKYLMMSYLVAYGDTVSAISG 866
 KLGASPQDILSENNEYGQNFTAASNLPVLIPVTLPLDIQSPSDEGRKRHIGLPLVIIGISLG 255
 + G + L N + T +LIP L PS + + + VI+G++ G
 Subject 867 RFGVDTERTLEANESELSEQDTINPTTLLIP-----LQNPPSSSQTIKTWVYVIVGVAAG 920
 Query 256 CTLLVVVSAILLVCVCLKMKSLSNRASSAET-----ADKLLSGVGSGVSKPTM 304
 LL+ + + V K K N + +E+ + + +S +
 Subject 921 VVLLLFFGYVIFVFKF-FRKTKKKNDQIAVSESFKPLEKPLKVEEHEFFESISSMAQSVKV 979
 Query 305 YETGAILEATMNLSEQCKIGESVYKANIEGKVLAVKRFKEDTEELKILQKVNHGNLVKL 364
 Y+ + AT N S C I SVY+ I+G + A+K+ +V+ E+ +L K+NH N++L
 Subject 980 YKFEELQSATDNFSPSCLIKGSVYRGITKGDLAAIKMDGNVNEITALLSKINHFNVIRL 1039
 MGVSDDNDGNCFVVVYEAENGSLLEEWLFAKSCSETNSRSRTSLWCQRISIAVDVSMGLQY 424
 G+ NDG+ ++V+EYA NGSL +W++ +N R L W QRI IA+DV+ GL Y
 Subject 1040 SGICF-NDGHWYLVHEYAVNGSLSDWIYNN-----NNDRRFLVWTQRIQIALDVATGLNY 1093
 MHEHAYPRIVHRDITSSNILLDSNFKAKIANFSMART----- 461
 +H H P +H+D+ S+N+L LD+F+AKIANF AR+
 Subject 1094 LHIHVSPSYIHKDMKSNVNLGDGFRAKIANFDQARSQAEQGEQFALTRHIVGKGYMAP 1153
 --FTNPMMMS-KIDVFAFGVVLIELLTGRKAMTTKENGEVVMLWKDIWKFIDQEEENREERL 518
 N + + S K+DV+AFGV++FE+ TG K+ GE + L + + + E++ +E+L
 Subject 1154 EYLENGLISTKLDVYAFGVMLEIFTG-KEVAALYGGESIHLSEVLAABL-HEDDGKEKL 1211
 RKWMDPKLDNYPIDYALSLASLAVNCTADKSLSRPTIAEIVLSLSLLTQPSPA 572
 ++DP LD YP + A+ + L +C RP + EIV SLS + S A
 Subject 1212 GDFIDPSLDGNYPPELAIFMIRLIDSCLTKAPAGRPMDEIVQSLSRILASSQA 1265

Score = 265 bits (676), Expect = 2e-68, Method: Compositional matrix adjust.
 Identities = 173/557 (31%), Positives = 293/557 (52%), Gaps = 56/557 (10%)
 Query 46 SCETYVTYISQSPNPLSLTSVSNIFDTSPLSIARASNLQHEEDKLIPGQVLLIPVTCGCT 105
 SC+ + + S+ P + + +S+S++ + P +A+ + + E + + +PV C C+
 Subject 74 SCQAFLIFRSEPP-YNDVSSISDLLGSDPSQLAQINSVD-ETATFETKKEVIVPVCSCS 131
 GNRSFANISYEINQGDSFYFVATTLYQNLTNWAVMDLNPGLSQFTLPIGIQVVIPLFCK 165
 G S AN SY + GD++ +A + + L+ + A+ L+ + G ++ +PL C
 Subject 132 GEFQSANTSYYVQHGDYTLIANNTFEGLSTCQALRSQRTSLLT-NIYTGTKLTVPRLCA 190
 CPSKNQLDRGIKYLITHVWQPNDNVFSVSNKLQASPQDILSENNYG-QNFTAASNLPVLI 224
 CP+RNQ D G+Y+L++ +D VS +S + G + L N QN P +
 Subject 191 CPTKNQSDVGVKYLMSYLVASGDYVSSISVRFGVDTGMTLEANELSEQN-----PNIY 243
 P-VTLLPDLIQSPSDGRKHIGLPLVIIGISLGC TL VVVSAILLVCVCLKMKSLSNRAS 283
 P TLL L PS + + + V+G+ G L+++ +++ K + A
 Subject 244 PFTTLLPQLQNPBSSSQTIKTWVYVYVAGSALVLLFGSVIFFKFFRKTRKTDPIAI 303
 S-----AETADKLSSGVSGYVSKPTMYETGAILEATMNLSEQCKIGESVYKANIE 333
 S E + L + S +Y+ + AT N S C+I SVY+ I+
 Subject 304 SESFEACEKPLKEEHEFLESISSIAQSLKVYKFEELQSATDNFPNCRIKGSVYRGTIK 363
 GKVLAVKRFKEDTEELKILQKVNHGNLVKLIMGVSSDNDGNCFVVYEAENGSLLEWLFA 393
 G + A+K+ +V+ E+ +L K+NH N++L G+ NDG+ ++V+EYA NG L +W++
 Subject 364 GDLAAIKMDGEVSNEIALLNKINHFNVIRLSCICF-NDGHWYLVHEYAVNGPLTDWIY- 421
 KSCSETNSRSRTSLTWQRISIAVDVSMGLQYMEHAYPRIVHRDITSSNILLDSNFRAKI 453
 + +SR L W QRI IA+DV+ GL Y+H + P VH+DI S N+L LD+S+F+RAKI
 Subject 422 ---NNNDDSRF-LVWMQRIOQIALDVATGLNLYLHSYTSPPYVHKDIKSGNVLLSDSFRAKI 477
 ANFSMART-----FTNPMMMS-KIDVFAFGVVLIELLTGRK 487
 ANF +AR+ N + +S K+DV+AFGV++E+LTG++
 Subject 478 ANFGLARSAAEQGEQFALTRHIGTRGYMAPEYLENGLVSTKLDVYAFGVLMEMLTGKE 537
 AMTTKENGEVVMLWKDIWKFIDQEEENREERL R KWMDPKLDNYPIDYALSLASLAVNCTA 547
 E GE + L D+ E + +E+LR ++DP L YP++ A+ + L +C
 Subject 538 VAALYE-GENMHL-PDVLVAVLHEGDGKEKLRNFIDPSLSGNYPLELAIVMIRLIDSCLK 595
 DKSLSRPTIAEIVLSLS 564
 SRP + EIV +LS
 Subject 596 KSPASRPDMVEIVQALS 612

>ref|XP_002990805.1| hypothetical protein SELMODRAFT_11326 [Selaginella moellendorffii]
 >b|EFJ08078.1| hypothetical protein SELMODRAFT_11326 [Selaginella moellendorffii]
 Length=539

Gene ID: 9659107 SELMODRAFT_11326 | hypothetical protein

[Selaginella moellendorffii]

Score = 275 bits (702), Expect = 2e-71, Method: Compositional matrix adjust.
 Identities = 187/552 (33%), Positives = 287/552 (51%), Gaps = 31/552 (5%)

Query 37	FSCPSNSPPSCETVVTYISQSPNFLSLTSVSNIFDTSPLSIARASNLQHEEDKLIPIPGQL	96
+SC SNS SC+ Y Y + + +L SV F S +A AS + + L+P QVL		
Sbjct 1	YSCVSNST-SCQAYAAYRALQGD--TLQSVGLRFLSVEQLAEASQIA-QSATLVPDQVL	56
Query 97	LIPVTCGCTGNRSFANISYEINQGDSFYFVATTLYQNLTNWHAVMDLNPGLSQFTLPIGI	156
LIP+ C C RS N +Y I GD+ Y V+ +Q LT + AV NP L G		
Sbjct 57	LIPLNCSASCGRSQFNATYIIQSGDTLYLVSNGTFQGLTTYQAVERANPLAVPTNLQPGD	116
Query 157	QVVIPLFCCKCPSKNQLDRGIKYLTHVWQPNDNVFSVSNKLGASPQDILSENNYQQNFTA	216
+V P+ C CPS Q+ G+ L+T+ P+ + ++ S + S+N + T		
Sbjct 117	SIVFFIRCACPSAQVAAGVTSLVTYSIWPGEILDGIARAWNVSRTTRLASDNTVSGSATL	176
Query 217	ASNLPVLIPVTLPLDIQSPSDGRKHRIGLPVIIGISLGCTLLVVSAILLVCVCLMKM	276
+ P S G+ +GI++ C V++ + LV + +		
Sbjct 177	SPAAPPANNPPNNSPSPDSSSSGSNTGM--YVGIAVACVAVALLVVVALIFYRRRSR	234
Query 277	SLNRASSAAETADK-----LLSGVSGYVS--KPTMYETGAILEATMNLSEQCKIGESV	327
+ ++S AE + + LL+G+ G V +P ++ + +AT N S I SV		
Sbjct 235	KVTKASSYAEPSKEQPSPHAPLAMHGHLVDSERPVVFSYEELCDATNNFSASHLIQGSV	294
Query 328	YKANIEGKVLAVKRKFEDVT-EELKILQKVNHGNLVKLMGVSSNDGNCFVVVEYAENG	386
Y+ + ++A+K K T +ELKIL KV+H NLVKL+G+ S +D F+VIEYA+NGS		
Sbjct 295	YRGILRKQLVAIKEKMGGTTSQELKILCKVHHSNLVKLIGICSGDD-KLFLVYEADNGS	353
Query 387	LEEWLFAKSCSETNSNRTSLWCQRISIAVDVSMGLQYMHAEHYPRIVHRDITSSNILLD	446
L SC + W R+ +A+DV+ GL+Y+H++ P VH+D+ SSNILLD		
Sbjct 354	LS-----SCLHNRTPAATAIWNTRLQVAMDVATGLEYIHDTKPSFVHKDVKSSNILLD	407
Query 447	SNFKAKIANFSMARTFTNP--MMSKIDVFAFGVVLIELLTGRKAMTTKENGEVVMLWKDI	504
+N +AK+ANF MAR + + +K+DV+AFGVVL+EL TGR+A+ + G D		
Sbjct 408	ANLRAKVANFGMARLYLTHGFVTTKVDVDYAFGVVLLEFTGREAILSTGTGSEKQYLADA	467
Query 505	W----KIFDQEENRE--ERLRKWMDPKLDNYYPIDYALSLASLAVNCTADKSLSRPTIAE	558
+ F ++N E E+L W DP LDN P D AL+ +A +C +RP + +		
Sbjct 468	FVKLTDGFGADDNEDEKIEKLKHADPILDNAVFWDIALNFVEVARSCVDADPDARPNMKD	527
Query 559	IVLSSLSSLTQPS 570	
+ LS L + S		
Sbjct 528	VTFKLSKLESS 539	

>**ref|XP_002974494.1|** hypothetical protein SELMODRAFT_11327 [Selaginella moellendorffii]
gb|EFJ24716.1| hypothetical protein SELMODRAFT_11327 [Selaginella moellendorffii]
 Length=539

GENE ID: 9657733 SELMODRAFT_11327 | hypothetical protein
 [Selaginella moellendorffii]-

Score = 273 bits (699), Expect = 4e-71, Method: Compositional matrix adjust.
 Identities = 187/552 (33%), Positives = 286/552 (51%), Gaps = 31/552 (5%)

Query 37	FSCPSNSPPSCETVVTYISQSPNFLSLTSVSNIFDTSPLSIARASNLQHEEDKLIPIPGQL	96
+SC SNS SC+ Y Y + + +L SV F S +A AS + + L+P QVL		
Sbjct 1	YSCVSNST-SCQAYAAYRALQGD--TLQSVGLRFLSVEQLAEASQIA-QSATLVPDQVL	56
Query 97	LIPVTCGCTGNRSFANISYEINQGDSFYFVATTLYQNLTNWHAVMDLNPGLSQFTLPIGI	156
LIP+ C C RS N +Y I GD+ Y V+ +Q LT + AV NP L G		
Sbjct 57	LIPLNCSASCGRSQFNATYIIQSGDTLYLVSNGTFQGLTTYQAVERANPLAVPTNLQPGD	116
Query 157	QVVIPLFCCKCPSKNQLDRGIKYLTHVWQPNDNVFSVSNKLGASPQDILSENNYQQNFTA	216
+V P+ C CPS Q+ G+ L+T+ P+ + ++ S + S+N + T		
Sbjct 117	SIVFFIRCACPSAQVAAGVTSLVTYSIWPGEILDGIARAWNVSRTTRLASDNTVSGSATL	176
Query 217	ASNLPVLIPVTLPLDIQSPSDGRKHRIGLPVIIGISLGCTLLVVSAILLVCVCLMKM	276
+ P S G+ +GI++ C V++ + LV + +		
Sbjct 177	SPAAPPANNPPNNSPSPDSSSSGSNTGM--YVGIAVACVAVALLVVVALIFYRRRPR	234
Query 277	SLNRASSAAETADK-----LLSGVSGYVS--KPTMYETGAILEATMNLSEQCKIGESV	327
+ ++S AE + + LL+G+ G V +P ++ + +AT N S I SV		
Sbjct 235	KVTKASSYAEPSKEQPSPHAPLAMHGHLVDSERPVVFSYEELCDATNNFSASHLIQGSV	294
Query 328	YKANIEGKVLAVKRKFEDVT-EELKILQKVNHGNLVKLMGVSSNDGNCFVVVEYAENG	386
Y+ + ++A+K K T +ELKIL KV+H NLVKL+G+ S +D F+VIEYA+NGS		
Sbjct 295	YRGILRKQLVAIKEKMGGTTSQELKILCKVHHSNLVKLIGICSGDD-KLFLVYEADNGS	353
Query 387	LEEWLFAKSCSETNSNRTSLWCQRISIAVDVSMGLQYMHAEHYPRIVHRDITSSNILLD	446
L SC + W R+ +A+DV+ GL+Y+H++ P VH+D+ SSNILLD		
Sbjct 354	LS-----SCLHNRTPAATAIWNTRLQVAMDVATGLEYIHDTKPSFVHKDVKSSNILLD	407
Query 447	SNFKAKIANFSMARTFTNP--MMSKIDVFAFGVVLIELLTGRKAMTTKENGEVVMLWKDI	504
+N +AK+ANF MAR + + +K+DV+AFGVVL+EL TGR+A+ + G D		
Sbjct 408	ANLRAKVANFGMARLYLTHGFVTTKVDVDYAFGVVLLEFTGREAILSTGTGSEKQYLADA	467
Query 505	W----KIFDQEENRE--ERLRKWMDPKLDNYYPIDYALSLASLAVNCTADKSLSRPTIAE	558
+ F ++N E E+L W DP LDN P D AL+ +A +C +RP +		
Sbjct 468	FVKLTDGFGADDNEDEKIEKLKHADPILDNAVFWDIALNFVEVARSCVDADPDARPNMKD	527
Query 559	IVLSSLSSLTQPS 570	
+ LS L + S		
Sbjct 528	VTFKLSKLESS 539	

>**ref|XP_002277331.1|** PREDICTED: hypothetical protein [Vitis vinifera]
 Length=638

GENE ID: 100258108 LOC100258108 | hypothetical protein LOC100258108
 [Vitis vinifera]

Score = 272 bits (696), Expect = 8e-71, Method: Compositional matrix adjust.
 Identities = 183/599 (30%), Positives = 298/599 (49%), Gaps = 82/599 (13%)

Query 31 QTNGTNFSCPSNSPPSCETYVTYISQSPNFLSITSVSNIFDTSPLSIARASNLQHEEDKL 90
 +TNG F C N P SC +Y+T+ S P++ S S++ + ++ P IA + + + D +
 Sbjct 32 ETNG--FQC--NGPRSCHSYLTFRSAPPYDSPPSIAYLLNSEPAQIATINEVS-DVDTI 86

Query 91 IPGOVLLIPVTCGCTGNRSFANISYEINQGDSFYF-VATTLYQNLTNWHAVMIDLNPGLSQ 149
 VL++EV C C+G+ N +Y+ YF +A+ YQ LT A+ NP
 Sbjct 87 SKDTVLIVPVCNSCGDFYQHNTTYTLKSASETYFSLANNTYQGLTTCQALKAQNP-YDY 145

Query 150 FTLP1GIVQVVIPLFCKCPSKNQLDRGIKYLITHVWQPNDNVSFVSNKLGASP-QDILSEN 208
 L +G+ + +PL C CP+ NQ G YL+ + + D + ++ G Q I N
 Sbjct 146 RNLSVGLHLQVPLMCAPCTANQTAAGFNLYLLSYLVWGDITDISIAKIFGVDDVQSIYDAN 205

Query 209 NYGQNFTAASNLPVLIPVTLPPDLIQS-----PSDGRKHRIGLPIIGIS 253
 P+L+P+ P IQ+ PS G + V IG
 Sbjct 206 RLSSTSVIVPFTPLVPLKNPPSKIQTTVSSPPAPSPETPMVPSGGGSNSSKKWVFIGAG 265

Query 254 LGCTLLVV-VSAIALLVCVCLMKMS-----LNRSASSAETADKLLSGVGSGY 298
 +G LLV+ +S+ ++ C + +S L+S + + L G+
 Sbjct 266 IGAALLVLLISSLGMFCFFRRRQSGQDKPVLDLGEATKLSKSLENKTSMSIISLEGIRIE 325

Query 299 VSKPTMYETGAIETATMLNQLEKIGESVYKANIEGKVLAVKFKFEDVTEELKILQKVNH 358
 +T+Y+ + + A E +I SVX+A+ +G A+K K DV+EE+ IL++FNH
 Sbjct 326 MESLTVYKYEELQKAAGYFGEANRIKGSVYRASFKGDDAAIKMMKGDVSEEINILKQINH 385

Query 359 GNLVLMGVSSNDGNCFVVYEAENGSLLEEWLFA---KSCSETNSNSRTSLWCQRISIAV 416
 +++L G + GN ++VYEAENG+L +WL ++CS +L W QR+ IA
 Sbjct 386 SKVIRLSGFCI-HAGNTYLVYEAENGALRDWLHGGETCS-----TLGWKQRVQIAY 437

Query 417 DVSMGLQYMHAYPRIVHRDITSSNILLDSNFKAKIANFSMARTFTNP----- 465
 D + L Y+H P +H++ SNIILD N + K+ NF +AR N
 Sbjct 438 DAADALNYLHNFSISSLPCIHKNLKLISNILLDGNGNMRGKVTFGLARRLGNEEGDGGGLQLTR 497

Query 466 -----MMSKIDVFAFGVVLIELLTGRKAMTT--KENGEVVMLWWDIW 505
 + K+D+FAFGVV+E+LLTG+A+ KE GE++ + I
 Sbjct 498 HVVGTQGYMAPEYVENGVVTPKLIDIFAFGVVILELLTGKEAAPSQKKEGGELLSV--SIN 555

Query 506 KIFDQEENREERLRKWMDPKLDNYYPIDYALSLASLAVNCTADKSLSRPTIAEIVLSSL 564
 ++ Q +N ++LR ++DP L + YP D A S+A LA +C A +RPT+++I + LS
 Sbjct 556 EVL-QGDNVRDKLRLGFIDPCLAHEYPFIDLAFSMAQLAKSCVAHDLNARPTMSDIFVILS 613

>**ref|XP_002269442.1|** PREDICTED: hypothetical protein [Vitis vinifera]
 Length=632

Gene ID: 100264999 LOC100264999 | hypothetical protein LOC100264999
 [Vitis vinifera]

Score = 268 bits (685), Expect = 2e-69, Method: Compositional matrix adjust.
 Identities = 182/611 (29%), Positives = 306/611 (50%), Gaps = 81/611 (13%)

Query 16 YVVLMMFFTCTIEAQSQQTNGTNFSCPSNSPPSCETYVTYISQSPNFLSITSVSNIFDTSPL 75
 Y ++ +TC NG N +C+TY+ +S+SP + ++S+S++ + P
 Sbjct 40 YTTVLGYTC-----NGVN-----TTCTQTYLIFRSESP-YNNVSSISDLLASDPS 82

Query 76 SIARASNLQHEEDKLIPGQVLLIPVTCGCTGNRSFANISYEINQGDSFYFVATTLYQNLT 135
 +A+ + ++ E + ++PV C C+GN S N SY + GD ++A +Q L+
 Sbjct 83 QLAQINSVT-ETATFDTNKEVIVPVNCSCSGNSYQNTNTSYVVKNGDYPYLWIANNTFQGLS 141

Query 136 NWHAVMDLNLPGSQTFLPIGIVQVVIPLFCKCPSKNQLDRGIKYLITHVWQPNDNVSFVSN 195
 A++ NP +S D L G + +PL C CP+K Q D G+KYL+ + + D VS +S
 Sbjct 142 TCQALLNQNPVSATNLPGTSITVPLRCACPTKAQSDAGVKYLMSYLVAYGDTVSAISG 201

Query 196 KLGASPQDILSENNEYGQNFTAASNLPVLIPVTLPPDLIQS-----PSD 238
 +G + L N + T +LIP+ P Q+
 Sbjct 202 RFGVDTERTLEANESELQDTINPTTLLIPLQNPSSSSQTIVPPPFPSSPAVSSPS 261

Query 239 GRKHIGLPIIIGISLGCTLLVVSAIILLCVCCCLKMKSLNRSSAET----- 287
 G + + VI+G+ G LL+ ++ V K K N + +E+
 Sbjct 262 GSSKKTWYVIVGVAAGVVLFFFYVIFVKF-FRKTKKKNDQIAVSESFKPLEKPLKVE 320

Query 288 ADKLLSGVSGYVSKPTMYETGAILEATMLNQLEKIGESVYKANIEGKVLAJKRFKEDVT 347
 + +S +Y+ +VY+ +AT N S C I SVY+ I+G + A+ + +V+
 Sbjct 321 EHEFFESISSMAQSVKYKFEELQSATDNFSPSCLIKGSVYRGTIKGDLAAIKKMDGNVS 380

Query 348 EELKILQKVNHNGLVLMGVSSNDGNCFVYVYEAENGSLLEWLFAKSCSETNSNSRTSLT 407
 E+ +L K+NH N++L G+ NDG+ ++V+EYA NGSL +W+ +N R L
 Sbjct 381 NEITALLSKINHFNVIRLGSICF-NDGHWYLVHHEYAVNGSLSDWIYYN----NNDRRFLV 434

Query 408 WCQRIISIADVSMGLQYMHAYPRIVHRDITSSNILLDSNFKAKIANFSMART----- 461
 W QRI IA+DV+ GL Y+H H P +H+D+ S+N+LLD +F+AKIANF AR+
 Sbjct 435 WTQRIQIALDVTAGLNLHIVPSVYIHKDMKSNVNLDDGDFRAKIANFDQARSQEGQEG 494

Query 462 -----FTNPMMMS-KIDVFAFGVVLIELLTGRKAMTTKENGEVVMLW 501
 N ++S K+DV+AFGV++E+ TG K + GE + L
 Sbjct 495 QFALTRHIVGTVKGYMAPEYLENLISTKLDVYAFGVIMLEIFTG-KEVAALYGGEIHL 553

Query 502 KDIWKIFDQEENREERLRKWMDPKLDNYYPIDYALSLASLAVNCTADKSLSRPTIAEIVL 561
 + + + E++ +E+L ++DP LD YP + A+ + L +C RP + EIV
 Sbjct 554 EVLAALV-HEDDGKEKLGFIDPLSDGNYPPELAIFMIRLDSLTKAPAGRPMDEIVQ 612

Query 562 SLSLLTQPSA 572
 SLS + S A
 Sbjct 613 SLSRILASSQA 623

>**dbj|BAI79276.1|** LysM type receptor kinase [Lotus japonicus]
 Length=633

Score = 268 bits (684), Expect = 2e-69, Method: Compositional matrix adjust.
 Identities = 204/659 (30%), Positives = 327/659 (49%), Gaps = 116/659 (17%)

Query 1 MAVFFVSLTLGQIILYVVLMMFFT-IEAQSQQTNGTNFSCPSNSP-PSCETYVTYISQSP 58
 + +F+ AQ Y+ L C S G ++C S +C+ Y-T+ +Q P
 Sbjct 14 LFIFTTFPITLAQQPYIGLATNACPRRGNSNSIRG--YTCNGGSANHTCQAYLTFRTQ-P 70

Query 59 NFLSLTSVSNIFDTSPLSIAR---ASNLQHEEDKLI PGQVLLIPVTCGCTGNRSFANIS 114
 + S+ ++S+ + +A + N E +KL+ ++PV C C G AN S

Subject 71 IYNSVYTISTLSSDARHLAETMSVSQNTTFETNKLV----IVPVQCSCAGEYYQANTS 125
 Query 115 YEINQGDSFYFVATTLYQNLTNWHAVM--DLNPGLSQFTLPIGQVVIPLFKCPSKNQL 172
 D+ + A ++ LT A+M + NPG L+G ++ +PL C CP+KNQ
 Subject 126 YAFQNTDTFFSIANNTFEGLTTCQALMHENHNPG---HLYLGRLELTVELRACACPTKNQT 181
 DRGIKYLITHWQPNDNVSFVSNSKLGASPDILSENNYQQNFTAASNLPLVILPVTLLPDL 232
 ++GIKYL+++ D+VS +S K G S + L N+ + T A P TLL L
 Subject 182 EKGIKYLLSYLVNWGDSVSVISKEFGVSCNNTLEANSL--SLTKAKIYPF---TTLLVPL 236
 IQSISDGR-----KHRIGLPIIIGISLGCCTLLVVVSAILLVC 269
 PS+ + ++ L V++G G L+V++A++ C
 Subject 237 HDKPSNSQTSILQSQPSSTSSPPSSSTHQSSNKTWLIVVVVG---GVFALIVLTAVIF-C 292
 VCCLMKMSLNRSASSAETAD-----KLLSGVSGYVSKPTMYETGAILEA 313
 + K+ + S S ++ KL + G +Y I A
 Subject 293 IHYHKGRKKDDSLSQLTVSEFNQQLGKEMKKGDGKLSEFIHGLAQSFKVYSFEEIQRA 352
 TMNLSEQCKIGESVYKANIEGKVLAVKRKFEDVTEELKILQKVNHNGLVKLMGVSSDNDG 373
 T NL+ I SVY+ G ++A+K+ DV+E++IL KVNH N++L GVS N+G
 Subject 353 TNNLNSSSLIKGSVYRGVMNGDLVAIKKTEGDSKEIQLNKVHSNVIRLSGVSF-NEG 411
 NCFVYYEAEAGSLEEWFALKSCSETNSRTSLTWCQRISIAVDVSMGLQYMHEAYPRI 433
 ++VYEYA NG L EW+F L+W QRI IA+DV++GL Y+H P
 Subject 412 QWYLVYEAANGPLSEWIFFGKF-----LSWTQRIQIALDVAIGLDYLSFTSPPH 462
 VRHDITSSNILLDSNFKAKIANFSMART-----FTNPM 466
 +H+D+ SSNILLDS+F+AKIAN S+AR+ N+
 Subject 463 IHKDLKSSNILLDSDFRAKIANLSLARSVKGVDEDQFLATRNIVGTRGYMAPEYLENGL 522
 MS-KIDVFAFGVVLIELLTGRK--AMTTKENGEVVMLWKDIWKFIDQEENREERLRKWM 523
 +S K+DV+AFGV++E+LTG++ A+ ++N K++ + EERL++MD
 Subject 523 VSTKLDVYAFGVIMLEILTGKEVAAILAEEDNN-----KNLGVLSAVLG-EERLKEFMD 575
 PKLDNYYPIDYALSLASLAVNCTADKSLSRPTIAEVILSLSLTQPSPATLERSLTSSG 582
 P L + YP + A+ + + V C SRP++ EIV +LS T S + E S+ SG
 Subject 576 PSLQSNYPFELAMFVFEIIVGCIIEKDPAASRPSMQEIVPTLS-RTMNSSLWEMSVNISG 633

>dbj|BAI79286.1| LysM type receptor kinase [Lotus japonicus]
 Length=633

Score = 267 bits (683), Expect = 3e-69, Method: Compositional matrix adjust.
 Identities = 203/659 (30%), Positives = 327/659 (49%), Gaps = 116/659 (17%)

Query 1 MAVFVFSLTLGAQILYVYVILMFFTC-IEAQSQQTNGTNFSCPSNSP-PSCETVYTYISQSP 58
 + +FF AQ Y+ L C S G + +C S +C Y+T+ +Q P
 Subject 14 LFIFTFPITLAQQPYIGLATNACPRRGNSNSIRG--YTCNGSANHTCQAYLTFRQ-P 70
 NFLSLTSVSNIFDTSPLSIAR----ASNLQHEEDKLIPGQVLLIPVTCGCTGNRSFANIS 114
 + S+ ++S + + A+ + N E +KL+ ++PV C C G AN S
 Subject 71 IYNSVYTISTLSSDARHLAETMSVSQNTTFETNKLV----IVPVQCSCAGEYYQANTS 125
 YEINQGDSFYFVATTLYQNLTNWHAVM--DLNPGLSQFTLPIGQVVIPLFKCPSKNQL 172
 D+ + A ++ LT A+M + NPG L+G ++ +PL C CP+KNQ
 Subject 126 YAFQNTDTFFSIANNTFEGLTTCQALMHENHNPG---HLYLGRLELTVELRACACPTKNQT 181
 DRGIKYLITHWQPNDNVSFVSNSKLGASPDILSENNYQQNFTAASNLPLVILPVTLLPDL 232
 ++GIKYL+++ D+VS +S K G S + L N+ + T A P TLL L
 Subject 182 EKGIKYLLSYLVNWGDSVSVISKEFGVSCNNTLEANSL--SLTKAKIYPF---TTLLVPL 236
 IQSISDGR-----KHRIGLPIIIGISLGCCTLLVVVSAILLVC 269
 PS+ + ++ L V++G G L+V++A++ C
 Subject 237 HDKPSNSQTSILQSQPSSTSSPPSSSTHQSSNKTWLIVVVVG---GVFALIVLTAVIF-C 292
 VCCLMKMSLNRSASSAETAD-----KLLSGVSGYVSKPTMYETGAILEA 313
 + K+ + S S ++ KL + G +Y I A
 Subject 293 IHYHKGRKKDDSLSQLTVSEFNQQLGKEMKKGDGKLSEFIHGLAQSFKVYSFEEIQRA 352
 TMNLSEQCKIGESVYKANIEGKVLAVKRKFEDVTEELKILQKVNHNGLVKLMGVSSDNDG 373
 T NL+ I SVY+ G ++A+K+ DV+E++IL KVNH N++L GVS N+G
 Subject 353 TNNLNSSSLIKGSVYRGVMNGDLVAIKKTEGDSKEIQLNKVHSNVIRLSGVSF-NEG 411
 NCFVYYEAEAGSLEEWFALKSCSETNSRTSLTWCQRISIAVDVSMGLQYMHEAYPRI 433
 ++VYEYA NG L EW+F L+W QRI IA+DV++GL Y+H P
 Subject 412 QWYLVYEAANGPLSEWIFFGKF-----LSWTQRIQIALDVAIGLDYLSFTSPPH 462
 VRHDITSSNILLDSNFKAKIANFSMART-----FTNPM 466
 +H+D+ SSNILLDS+F+AKIAN S+AR+ N+
 Subject 463 IHKDLKSSNILLDSDFRAKIANLSLARSVKGVDEDQFLATRNIVGTRGYMAPEYLENGL 522
 MS-KIDVFAFGVVLIELLTGRK--AMTTKENGEVVMLWKDIWKFIDQEENREERLRKWM 523
 +S K+DV+AFGV++E+LTG++ A+ ++N K++ + EERL++MD
 Subject 523 VSTKLDVYAFGVIMLEILTGKEVAAILAEEDNN-----KNLGVLSAVLG-EERLKEFMD 575
 PKLDNYYPIDYALSLASLAVNCTADKSLSRPTIAEVILSLSLTQPSPATLERSLTSSG 582
 P L + YP + A+ + + V C SRP++ EIV +LS T S + E S+ SG
 Subject 576 PSLQSNYPFELAMFVFEIIVGCIIEKDPAASRPSMQEIVPTLS-RTMNSSLWEMSVNISG 633

>ref|XP_002533279.1| serine-threonine protein kinase, plant-type, putative [Ricinus communis]
 gb|EEF29111.1| serine-threonine protein kinase, plant-type, putative [Ricinus communis]
 Length=617

Gene ID: 8272991 RCOM_0411670 | serine-threonine protein kinase, plant-type, putative [Ricinus communis]

Score = 264 bits (674), Expect = 3e-68, Method: Compositional matrix adjust.
 Identities = 179/580 (30%), Positives = 309/580 (53%), Gaps = 74/580 (12%)

Query 37 FSCPSNSPPSCETVYTYISQSPNFLSLSLTSVSNIFDTSPLSIARASNLQHEEDKLIP-GQV 95
 ++C N SC+T++ Y SQ P + ++S+S + + PL +A +N+ + ++P +
 Subject 47 YTC--NGKECSCKTFLIYKSQPP-YHTVSSISKLTSSTDPLEALINNISNF--TVLPTNKE 101
 LLIPVTCGCTGNRSFANISYEI-NQGDSFYFVATTLYQNLTNWHAVMDLNPGSQFTLPI 154

Sbjct 102 +++P+ C C+ AN SY I + D+++ +A + Y+ L+ +++M N S+F+L + VIVPIICSCSSQQYQANTSYIIPSIYDTYFSIAESTYEGLSTNSLMRQN-NYSEFSLDV 160

Query 155 GIQVVIPLFCKCPSKNQLDRGIKYLITHVWQPNDNVSFSNKILGASPQDILSENNYQONF 214
G+++ +PL C CP+ NQ G KYL+T+ D V VS + AS + NY F

Sbjct 161 GMELRVPLRCACPTSNSQSANGTKYLLTYSVSGDKVRASERFNASIDSV---NYANGF 216

Query 215 TAAASN--LP---VLIPVTLLPDLIQS-----PSDGRKHRIGLGPVI 249
T P +L+P++ P Q+ S + H +FVI

Sbjct 217 TKDDTTLFFFTTILVPLSTEPSSFQTIVHYPFFFFSPPFIPVHPIRRSRKKIHVVWVPIVVI 276

Query 250 IGISLGCTLLVVVSAIILVCVCLMKMSLNRSASSAETADKLLSGVSGVSKPTMYETGA 309
I +L L +V+ +L D ++ E D L V+ +Y

Sbjct 277 IVSALPVVLFIVL--LLRNKKSMLGVQREKEGKNEELPDDFLDHVAHVDLGLKIYTFEE 334

Query 310 ILEATMNLSEQCKVANIEGKVLAVKRKEDVTEELKILQKVNHGNLVLGMVSS 369
+ AT + S ++ +SVY+ I G+VLA+K+ +DV+ E+ +L+K+NH NL+ L +

Sbjct 335 LKVATEDFSTSNSRLSDSVYRGVISGQVLAIKKMSKDVSNEVTLRKINHFNLISHA-AC 393

Query 370 DNDGNCFVYYEYAENGSELLEFWFAKSCSETNSNRTSLWCQRISIAVDVSMGLQYMHEHA 429
++ G ++YE+ +NGSL +WL+ ++C E +W +RI IA+DV+ GL Y+H

Sbjct 394 EHGFVYLMYEFMDNGSLRDWLYKRNCLEAQ----SWNRRIQIALDVALGHLYHNFT 447

Query 430 YPRIVHRDITSSNILLDSNFKAKIANFSMART-----FTNP----- 465
P VH+DI+SSN+LL + +AKIANFS+AR+ + P

Sbjct 448 DPYVHKDISSSNVLLSRLRAKIANFSLARSAKAEHVNSSLLRALGSKGYLAPEFIDF 507

Query 466 --MMSKIDVFAGVVVLIELLTKRANKMTTENGEVVMLWVKDIDWKFIDQEEENREERLRKWM 523
+ +ID+ +AFGVVL+L+TG+A+ +E -V L+ I I ++E N E RL +D

Sbjct 508 GLVTPEIDIYAFGVVLLLELTGEAVYMQEERKV-QLSETIISIMEKE-NAEARLGCIVD 565

Query 524 PKLDNYYPIDYALSLASLAVNCATDKSLSRPTIAEIVL 563
P L + + ++ L + L++ C A + SRP+AEIV +L

Sbjct 566 PNLIQSQHSMEVVLRMVKLSLACLAQEPESRPSMAEIVSAL 605

>**ref|XP_002533278.1|** BRASSINOSTEROID INSENSITIVE 1-associated receptor kinase 1 precursor, putative [Ricinus communis]
gb|EEF29110.1| BRASSINOSTEROID INSENSITIVE 1-associated receptor kinase 1 precursor, putative [Ricinus communis]
Length=647

Gene ID: 8272990 RCOM_0411660 | BRASSINOSTEROID INSENSITIVE 1-associated receptor kinase 1 precursor, putative [Ricinus communis]

Score = 263 bits (673), Expect = 4e-68, Method: Compositional matrix adjust.
Identities = 187/626 (29%), Positives = 314/626 (50%), Gaps = 95/626 (15%)

Query 18 VLMFCTCIEAQSQD----TNGTN-----FSCPNSPPSCETYVTYISQSPNFLSL 63
+ + F C+ +QO TN TN +SC + SC+TY+T+ SQ P + ++
Sbjct 14 IFIACFCCLLIHAQQPYVAKATTNTNTADSALGYSC-NGLNTSQCPTYLTFRSQQP-YTNV 71

Query 64 TSVSNIFDTSPLSIARASNLQHEEDKLIPQVLLIPVTCGCTGNRSFANISYEINQGDF 123
TS+S + ++ P ++ A N E +++++PV C C+G+ AN SY + D+
Sbjct 72 TSISTLNSDPSQLS-AINSVSETATFDTNKLVIVPVNCSCSDYYQANTSYVVQAKDAP 130

Query 124 YFVATTLYQNLNTWHAVMDLNPGLSQFTLPIGIGQVVIPLFCKCPSKNQLDRGIKYLITHV 183
+F+A +Q L+ A+ D N + P I + IPL C CP+KNO D GIKYL+++
Sbjct 131 FFIANTNTFQGLSTCQAINDNQRQTVDFIPNEMI-LHIPLRCACPTKNQTDAGIKYLLSYL 189

Query 184 WQPNNDNSVFSVNLKGASPQDILSENNYQ-QNFTAASNLPLVLPVTLPPDLIQS----- 235
D VS VS K G+ L N Q T +LIP+ P Q+
Sbjct 190 VTWCDTVAWSVFKGGNTGRSLEANGLSEQTPTIYPFTTLLIPLENPPTSNQDISPPPPP 249

Query 236 -----PSDCRKHRIGLIVIIGISLGCTLLVVVSAIILVCVCC----- 272
P+G + + V++G+ G + + I+ +
Sbjct 250 ASSPPPPPSTDTPNNGSSKKWVYVVLGVLAGIVFTLGLVTTIIFYALFRRSKRKPEPIIV 309

Query 273 -----LKMKSLSNRSASSAETADKLLSGVSKPTMYETGAIATEATMNLSSEQCKIGESV 327
+ KSLN+ E + L +S + X+ + AT N S C I SV
Sbjct 310 SESFEAQEKSLSNKKL--EESQDFLDSISSIAQSIKVKFKELEATDNFSPSCWIKGSV 367

Query 328 YKANIEGKVLAVKRFKEDVTEELKILQKVNHGNLVLGMVSSDNDGNCFVYYEYAENGSL 387
Y+ I G A+K+ DV+E++L KVNH NL++L GV G+ ++VYEYA NG+L
Sbjct 368 YRGYISGDXAAIKKVNGDVSKEIELLNKVNHFNLIRLSGVCFSG-GHWLVYEAANGAL 426

Query 388 EEWLFAKSCSETNSNRTSLWCQRISIAVDVSMGLQYMHEAYPRIVHRDITSSNILLDS 447
+W++ +N L+W QR+ IA+DV+ GL Y+H P +H+DI SSN+L+DS
Sbjct 427 SDWIYY-----SNNEGFLSWTQRVQIALDVTAGLNYLHSFTSPPHIHKDIKSSNVLIDS 481

Query 448 NFKAKIANFSMART-----FTNPMMMS-KIDVFAGVVVIE 481
+F+AKIAN +MAR+ N ++S K+DV+AFG+++=E
Sbjct 482 DFRAKIANLAMARSTEGQDGFEFALTRHIVGTKGYMAPEYLENLVSTKLDVYAFGILMLE 541

Query 482 LLTGRK--AMTTKENGEVVMLWVKDIDWKFIDQEEENREERLRKWDMPKLDNYYPIDYALSLA 539
++TG++ A+T+EN + + D+ +E+ ++ L+ ++DP ++ +P + +L +
Sbjct 542 MVTGKEVAALYTEENLNLSIDLNDVLS---KEDGQQSLKQFVDPMSMEENFPSEISLFMM 597

Query 540 SLAVN-CTADKSLSRPTIAEIVL 564
++ C RP + EI SLS
Sbjct 598 VRMIDSCLNKNPADRPAMDEISQSL 623

>**ref|XP_002522569.1|** BRASSINOSTEROID INSENSITIVE 1-associated receptor kinase 1 precursor, putative [Ricinus communis]
gb|EEF39869.1| BRASSINOSTEROID INSENSITIVE 1-associated receptor kinase 1 precursor, putative [Ricinus communis]
Length=624

Gene ID: 8259229 RCOM_1014860 | BRASSINOSTEROID INSENSITIVE 1-associated receptor kinase 1 precursor, putative [Ricinus communis]

Score = 262 bits (669), Expect = 1e-67, Method: Compositional matrix adjust.
Identities = 180/601 (29%), Positives = 304/601 (50%), Gaps = 69/601 (11%)

Query 25 IEAQSQQTNGTNFSCPSNSPP-----SCETYVTYISQSPNFLSLSVSNIFDTS 73

Sbjct	24	+EAQ + C + P SC++Y+T+ + P + S + + + LEAQQAYVDNHLQDCHDSDPSTKGVLNCNGVQSSCQSYITFRANPP-YNSPAKIGYLLGSQ	82
Query	74	PLS--IARASNLIQHEEDKLIPGQVLLIPVTCGCTGNRSFA-NISYEI-NQGDSFYFVATT + IA +N+ + + + +PV C C + N +Y I ++ +++++ +A	129
Sbjct	83	SEATLIASMNNISCDVATIPTNKQVVVPNCSCAGLQQHNAATYRIKDENENYFTILAND	142
Query	130	LYQNLTNWHAVMIDLNP-GLSQFTLPIGIQVVIPLFCCKCPSKNQLDRGIKYLITHVWQPND YQ LT ++ + NP L++ L G + +PL C CP+ NQ G+K ++T+ +D	188
Sbjct	143	TYQGLTTCQSLWEQNPYDLNE--LYAGSDLHVPLRCACPTNPQTASGVKCMITYMVWTGD	200
Query	189	NVSFVSNKLGASPDILSENNYGCNFTAASNLPVLIIPVTLPLDIQ---SPSDGRKHRI +S ++ A+ Q +L N ++ P+L+P+ P + SP R +	244
Sbjct	201	YISLIAELFNANEQSVDANELLEDLIYPFTIPVPLLSEPTVLDLPGYSPPPTRTPPV	260
Query	245	G-LV-----IIGISLGCTLLVVV--SAILLVCVCC-LMKSLNRASSAETADK PV G +G LLV+V SA C KS +AT + +	290
Sbjct	261	EVFPVTESSNSKWKVFFGTGIGAVLLVLVAFAFSFWYFCRRPSQKSQEPNATKTDPPSV	320
Query	291	LLSGVSGYVSKPTMYETGAILEATMNLSEQCKIGESVYKANIEGKVLAJKRKFEDVTEEL G+ ++ +Y+ +I AT N SE ++ SVYK EG AVK + DV+ E+	350
Sbjct	321	SHVGIEFFIESLIIYKFDTSIQTAGNFSEDNRVKGSVYKGIFEGDHAALKAMRGDVSEI	380
Query	351	KILQKVNHGNLVKLMGVSSDNDGNCFVYYEYAENGSLLEEWLFAKSCSETNSRTSLTWCQ IL+K+NH N+V+L G ++GN ++VY+YAENGSL+WL S +SL+W Q	410
Sbjct	381	DILKKMMNHSNIVRLSGFCV-HEGNTLYLVQYAENGSLDDWLHLYKNDPVS---SSLSWKQ	436
Query	411	RISIAVDVSMGLQYMHEHAYPRIVHRDITSSNILLDSNFKA KIANFSMARTFTN----P R+ IA +V+ Y+H + P VH++T+SNILL NF+A I NF +AR +N P	465
Sbjct	437	RLQIAYNVADAFTYLNHNTTPFVHKNLTTSNILLHGNGFRAMITNGFLARKLNSDDQGAP	496
Query	466	MMS-----KIDVFAFGVVLIELLTGRKAMTTKENGEVVMLWKD + + K+DVFA+GVV++ELL+G+KA+ ++ NGE ML+	503
Sbjct	497	QLTRHVGTVGNGYMAPEYLENGLITPKLDFVAYGVVILELLSGKAVMSETNGEEKMLFAL	556
Query	504	IWKIFDQEENREERLRKWMDPKLDNYYPIDYALSLASLAVNCTADKSLSRPTIAEIVLSL I + + +N E+L+ ++DP L P+ +A S+A LA +C A RP++ E+ +SL	563
Sbjct	557	INNVL-EGDNVREKLAFIDPCRLGNIPLHFAFSIAQLAKDCVAHDPNDRPSMLEVFMSL	615
Query	564	S 564	
Sbjct	616	S 616	

>**emb|CBI40796.3| unnamed protein product [Vitis vinifera]**
Length=680

Sort alignments for this subject sequence by: E value Score Percent identity Query start position Subject start position			
Score = 259 bits (661), Expect = 9e-67, Method: Compositional matrix adjust. Identities = 171/526 (32%), Positives = 280/526 (53%), Gaps = 35/526 (6%)			
Query	57	SPNFLSLTSVNIF--DTSPSLSIARASNLIQHEEDKLIPGQVLLIPVTCGCTGNRSFANIS S +F + S+S+ + ++P IA + + + +K+ VL++PV C C+G+ N S	114
Sbjct	137	SDDFQASGSLSHAYLLNSNPSDIATINQIS-DVNKIPKDTVLIVPVNCSCSGHFYQYNAS	195
Query	115	YEINQGDSFYF-WATTLYQNLTNWHAVMDLNPGLSQFTLPIGIQVVIPLFCCKCPSKNQLD Y + YF +A YQ LT A+ NP + L +G+ ++PL C CP+ NQ	173
Sbjct	196	YTLYKDFENYFTLANNTYQGLTTCQALKAHNPYYYR-NLSVGMDDLVLPLMCAPTAQTA	254
Query	174	RGIKYLTHVWQPNDNVSFVSNLKGASP-QDILSENNYGCNFTAASNLPVLIIPVTLPLDL G YL+T++ D +S +++ G Q I N+ + +P+L+P+ P	232
Sbjct	255	AGFNYLLTLYLWTWGDYISSIADTFGVDDIQSIFDANSISSLSDLIIFPFT-PILVPLKNPPTR	313
Query	233	IQSP-----SDGRKHRIGLPVIIIGISLGCTLLVVV--SAILLVCVCC LKMDSL IQ+ + G V +G+ +TLLV++ S I+L C K S	278
Sbjct	314	IQTTLSPPPPSPVVPNGGADSSKKWVYVGVGIGATLLVLMPSGII-----CTKKPSY	369
Query	279	NRSASSAETADKLLSGVGSGYVSKPTMYETGAILEATMNLSEQCKIGESVYKANIEGKVL + + + + G+ V T+Y+ + +A E +I VY+ I+G A	338
Sbjct	370	SMENNISLSVSS--GGIHHAVESLTVYKYEELQKAAGFFGEANRIKGCVYRGLIKGDDAA	427
Query	339	VKRKFEDVTEELKILQKVNHGNLVKLMGVSSDNDGNCFVYYEYAENGSLLEEWLFAKSCSE +K K DV+EE+ IL+ +NH N++L G + GN ++VYEAENGSL +WL	398
Sbjct	428	IKMMKGDVSEEINLKLINHNSNIVRLSGFCV-HKGNTLYLVEYEAENGSLSDWLHGDG---	483
Query	399	TSNSRTSLTWQCIRISIAVDVSMGLQYMHEHAYPRIVHRDITSSNILLDSNFKA KIANFSM ++L W QR+ IA DV+ L Y+H P +H++ SSNILLD N + K+ANF +	458
Sbjct	484	--RIGSTLQWKQRVQIACDVANALNLYLHNFTNPPCIHKNLKSSNILLDGNMRGKVAHFGL	541
Query	459	ARTFTNPMMSKIDVAFGVVLIELLTGRKAMTTKENGEVVMLWKLWDIWKIFDQEENREERL AR N ++D FAFGV++ELLTG+A + +N E L + + + +R +L	518
Sbjct	542	ARRLENEEGGELDAFAFGVVI ELLTGKEAAPS-QNKEGRGLCVSNEVLEGDDVR-HKL	599
Query	519	RKWMKPDKLDNYYPIDYALSLASLAVNCTADKSLSRPTIAEIVLSSL R ++D L + YP D A ++A LA +C A +RPT+ +I+ LS	564
Sbjct	600	RGFIDPCCLTHDYPFDLAFTMAQLAKSCIAHDLNARPTMFIDILI LS	645

Score = 77.4 bits (189), Expect = 5e-12, Method: Compositional matrix adjust.
Identities = 43/98 (43%), Positives = 66/98 (67%), Gaps = 5/98 (5%)

Query	469	KIDVFAFGVVLIELLTGRKAMTT--KENGEVVMLWKLWDIWKIFDQEENREERLKRWMKPDKL K+D+FAFGV++ELLTG+A + KE GE +L I ++ Q +N ++LR ++DP L	526
Sbjct	31	KLDI FAFGVVILELLTGKEAAPSQKKEGGE--LLSVS1NEVL-QGDNVRDKLRFIDPCL	87
Query	527	DNYYPIDYALSLASLAVNCTADKSLSRPTIAEIVLSSL + YP D A S+A LA +C A +RPT++I + LS	564
Sbjct	88	AHEYPFDLAFMSAQLAKSCVAHDLNARPTMSDIFVILS	125

>**ref|XP_002510333.1| Ricinus communis serine-threonine protein kinase, plant-type, putative**
>**gb|EEF52520.1| Ricinus communis serine-threonine protein kinase, plant-type, putative**

Length=637

GENE ID: 8260932 RCOM_1593420 | serine-threonine protein kinase, plant-type, putative [Ricinus communis]

Score = 258 bits (658), Expect = 2e-66, Method: Compositional matrix adjust.
 Identities = 164/557 (29%), Positives = 294/557 (52%), Gaps = 53/557 (9%)

Query 46	SCETYVTYISQSPNFLSLSLTSVSNIFDTSPLSIARASNLQHEEDKLIPGQVLLIPVTCGCT	105
Sbjct 54	TCQAFLIFRSRPP-YDSAPTISALTSASQEELARFNNVTGLSEFPLNKEVI-VPVSCSCL	111
Query 106	GNRSFANISYEINQGDSFYFVATTLYQNLTNWAVMDLNPGLSQFTLPIGIQVVIPLFCK	165
Sbjct 112	G AN S++ S+ Y+ L+ ++ N +F L+ G++ +PL C GQYYQANTSFQVASDHSYFTIASQTYEGLSTCASKKANI-YGEFDLALGAEQVPLRCA	170
Query 166	CPSKNQLDRGIKYLITHWQPNNDNSFSVSNKLGASPQDILSENNYQGNFTAASNLPVLIP	225
Sbjct 171	CP+ +Q+ KYL+T +D+++ ++ S+ I+ N++ T+ +LIP CPTASQVRNETKYLTFPISESNDHIAAIAERFNVSKESIIDANGLRESPTIYDTTLIP	230
Query 226	VTLPLDIQ-----SPSDGRKHRIGLPVIIGISLGCTLLVVSAILLVCV	270
Sbjct 231	+T P Q SP D R+ +L +G+ C+LLV+ +I++V + LTTEFSNSQTIIHENPTEVSPPASPPDNRRSRKLYEKVGITAACSSLVL--SIVVIL	288
Query 271	CCLKMKSLNR--SASSAETADKLLSGVSGYVSKPTMYETGAILEATMNLSEQCKIGESVY	328
Sbjct 289	L+ ++ + + L ++ ++ + + +AT N S+ I S+Y FLLRKDRRHKFPEINRRREQEDLRLIEASVEQVLKVFGLEEVKKATDNFSSKHIKGSLY	348
Query 329	KANIEGVKLVAKRFKEDVTEELKILQKVNHNGLVKLMGVSSDNDGNCFVVYEANGSLE	388
Sbjct 349	G++LA+K+ DV++E+ IL++NH NL+KL GV +N G ++ +EY +NGSL+ WGEFNGQILAIKKMNNDVSKEVNVILKRINHNFLNLHGVC-ENLGCFYLFEEYMKNGSLQ	407
Query 389	EWLFAKSCSETNSRTSLTWCQRISIAVDVSMGLQYMHEAYPRIVHRDITSSNILLDSN	448
Sbjct 408	EWL + + +W QRI IA+D++ GL Y++ P VH+DITS +ILLD+N EWLSRERFEDVGG----SWNRIQIALDIANGLFYLSHTEPACVHKDITSGHILLDNN	461
Query 449	FKAKIANFSMARTFTNPMM-----KIDVFAFGVVLIELLTGR	486
Sbjct 462	+AKIANFS+AR N +++ KIDV+AFG+V+EL+TG+ LRAKIANFSLARAANAVLTKHIEGTRGYMAPEYVQAGQVTPKIDVYAFGIVLLELITGK	521
Query 487	KAMTTKENGEVVMWLWDKIFDQEEENREERLRKWMDPKLDNYYPIDYALSLASLAVNCT	546
Sbjct 522	At ++ G+ +L K I+ + ++ EN E L +DP AL LA ++ C DAVFMRD-GKETILLSKAIFSVMEK-ENAAEALAFVIDPSFTGGRQSKLALRARIARVSLACL	579
Query 547	ADKSLSLRPTIAEIVLSL 563	
Sbjct 580	RP++ E+V +L TQVPARRPSMGEVVSTL 596	

>**ref|XP_002269408.1|** PREDICTED: hypothetical protein [Vitis vinifera]
 Length=638

GENE ID: 100242712 LOC100242712 | hypothetical protein LOC100242712
 [Vitis vinifera]

Score = 256 bits (653), Expect = 9e-66, Method: Compositional matrix adjust.
 Identities = 171/574 (29%), Positives = 292/574 (50%), Gaps = 66/574 (11%)

Query 46	SCETYVTYISQSPNFLSLSLTSVSNIFDTSPLSIARASNLQHEEDKLIPGQVLLIPVTCGCT	105
Sbjct 54	SC+ ++ S+ P + ++S++ + P +A+ +++ E + +++FV C C+ SCQAFLIFRSRSEPP-YNDVSSISDLGSDPSQLAQINSVD-ETATFETKKEVIVPVNCSCS	111
Query 106	GNRSFANISYEINQGDSFYFVATTLYQNLTNWAVMDLNPGLSQFTLPIGIQVVIPLFCK	165
Sbjct 112	G S AN SY + GD++ +A ++ L+ A+ L+ + G ++ +PL C GEFSQANTSIVVQHQDTYLLIANNTFEGLSTCQLRSQRTSIT-NIYTGTKLTVPLRCA	170
Query 166	CPSKNQLDRGIKYLITHWQPNNDNSFSVSNKLGASPQDILSENNYQ-QNFTAASNLPVLIP	224
Sbjct 171	CP+KNQ D G+KYL+ +++ D VS + S + G L N QN +LI CPTKNQSDVGVKYLMSYLVASGDYVSSISVRFVGDTGMLEANELSEQNPNIYFTTLLI	230
Query 225	PTVLLPDLIQ-----PSDGKRKHRIGLPVIIGISLGCTLLVVSAIL	266
Sbjct 231	P+ LP Q+ + + V++G+ G L++ ++ PLQNLPLSSSQTIVPPPSSSSSSPPPTAVSSPSKSLKKTWVYVVVGVVAGSALVLLFGSVI	290
Query 267	LVCVCCLKMKSLNRSASS-----AETADKLLSGVSGYVSKPTMYETGAILEATMN	316
Sbjct 291	K + A S E + L +S +Y+ + AT N FFKFFRKTRKTDPIAISESFEACEKPLKEEQHEFLEISSIAQSLKVYKFEELQSATDN	350
Query 317	LSEQCKIGESVYKANIEGVKLRFKEDVTEELKILQKVNHNGLVKLMGVSSDNDGNCF	376
Sbjct 351	S C+I SVY+ I+G + A+K+ +V+ E+ +L K+NH N++L G+ NDG+ + FSPNCRIKGSVYRGTIKGDLAAIKKMDGEVSNEIALLNKINHNFVINRLSGICF-NDGHWY	409
Query 377	VVYEYAENGSLLEWLFAKSCSETNSRTSLTWCQRISIAVDVSMGLQYMHEAYPRIVHR	436
Sbjct 410	+V+EYA NG L -W++ + SR L W QRI IA+DV+ GL Y+H + P VH+ LVNEYAVNGPLTWIY---NNNDDSRF-LVWMQRIOQIALDWTGNYLHSYTSPPYVHK	464
Query 437	DITSSNILLDSNFKAKIANFSMART-----FTNPMMS-KI	470
Sbjct 465	DIKSGNVLLSDSFRAKIANFGLRSAEGQEGQFALTRHIIGTRGYMAPEYLENGLVSTKL	524
Query 471	DVAFGVVLLIELLTGCRKAMTTKENGEVVMLWKD1WKFQEEENREERLRKWMDPKLDNYY	530
Sbjct 525	DV+AFGV++E+LTG+ + E GE + L D+ E + +E+LR ++DP L Y DVYAFGVMLLEMILTGKEVAALYE-GENNMLH-PDVLVAVLHEGDGKEKLRFNIDPSLSGNY	582
Query 531	PIDYALSLASLAVNCTADKSLRPTIAEIVLSL 564	
Sbjct 583	P++ A+ + L +C SRP + EIV +LS PLELAIVMIRLIDSLCKSPASRPDMVEIVQALS 616	

>**ref|XP_002281880.1|** PREDICTED: hypothetical protein [Vitis vinifera]
 Length=622

GENE ID: 100248852 LOC100248852 | hypothetical protein LOC100248852
 [Vitis vinifera]

Score = 254 bits (650), Expect = 2e-65, Method: Compositional matrix adjust.
 Identities = 188/608 (30%), Positives = 305/608 (50%), Gaps = 83/608 (13%)

Query 23 TCIEAQSQQTNGTNFSCPS--NSPPS-----CETYVTYISQSPNFLSLTSVS 67
 Sbjct 16 +CI AQ + + + C + + S PS C+ ++ + S+ P+ S+ ++S SCINAQQEYSGNSVLCNSDDSGPSSAFLYTCNGLYSSCQAFLIFKSEPP-YNSVPTIS 74

Query 68 NIFDTSPLSIARASNLQHEEDKLIP-GQVLLIPVTCGCTGNRSFANISYEINQGDSFYFV 126
 Sbjct 75 + ++P +AR +++ + + P G+ ++PV C C G AN ++ I YF+ MLMSSNPGEELARINSVK--TLTVFPTGKEVIVPVCNSCLGQYYQANTTFHICDQNQQTYFI 132

Query 127 -ATTLYQNLNTNWAVMDLNPGLSQFTLPIGIQVVIPLFCKCPSKNQLDRGIKYLITHWQ 185
 Sbjct 133 YQ L+ ++M N S+F+L G+++. +PL C C +++Q + G KYL+T+ IGNNTYQGLSTCDLMLRAN-RYSEFSLSPGLELHVPILRCACHTEHQAENGTKYLITYSVS 191

Query 186 PNDNVSFSVNKLGLASPQDILENNY---GQNFTAASNLPVLIPTLPLDIQ----- 234
 Sbjct 192 DN + + S+ I N +N T +LIP+ P Q WEDNFPTIGERFNVSAKSIADANGLISEENPTIFPFTTILIPKTEPLSSQTKTHATQPV 251

Query 235 -----SPSDGRKHRIGLPVIIGISLGCTIL--VVVASAILLCVCCMKSLNRSA 282
 Sbjct 252 S S K RI L GI+ GC LL V+ S + L K LDPPPSTSMSGSSRSRKRIYLGAA-GIAAGCFLLGPSVIFSIVFLFYKKRSKVPPVHKG 309

Query 283 SSAETADKLLSGVSGYVSKPTMYETGAALLEATMNLSECKIGESVYKANIEGVLAVER 342
 Sbjct 310 + + + LL ++ P ++E + +AT N S + +I V++A + + +AVK+ TKSVLPEDLLVETIASVDPVPKVFEFKKLKATGNFSSKSRIKGCVFRAELGREIVAVKMM 369

Query 343 KEDVTEELKILQKVNHNGLVKNVGSVSSDNDGNCF-VVVEYAENGSLPEEWLFAKSCSETSN 401
 Sbjct 370 K D++EE+ IL K+NH NL+KL GV +G+CF +V+EY ENGS ELW +S KVDIRSEEVNILNKLNCNLIKHLHGVC--KNGSCFYLVFEMENGSRLREWLHKES---- 421

Query 402 SRSTLTWCQRISIAVDVSMGLQYMHEHAYPRIVHRDITSSNILLDSNFKAKIANFSMART 461
 Sbjct 422 S S +W +RI IA+DV+ GL Y+H P VH+ I SSNILL N +AKIANFS+ART SNHSQSWSKRIQIALDVANGLHYIHNFTKPAYVHKHICKSSNILLTKNLRAKIANFSLART 481

Query 462 -----FTNP-----MMSKIDVFAFGVVLIELLTGRKAMTTKENG 495
 Sbjct 482 + P + K+DV+AFGVV+EL+TG+ A+ +N AVKGAKTHALNMLVVGTRGYMAPEYIEAGSITPKVDVYAFGVVMMLEITGKDAAVII-QNE 540

Query 496 EVVMLWKDIWIQDFQEENREERLRKWMDFPKLDNYPIDYALSLASLAVNCTADKSLSRPT 555
 Sbjct 541 E E V+L + + I ++ N E L ++DP L I+ A +A L++ C RP+ EEVLLSEAMISIMER-GNAEIELGHFLDPCLLGNNGIESATRIAKLSIACLTKDQARRPS 599

Query 556 IAEIVLSL 563
 Sbjct 600 MGEVVSTL 607

>**ref|XP_002310777.1|** predicted protein [Populus trichocarpa]
gb|EEE91227.1| predicted protein [Populus trichocarpa]

Length=643
GENE ID: 7477999_POPTRDRAFT_563086 | hypothetical protein [Populus trichocarpa] (10 or fewer PubMed links)

Score = 253 bits (645), Expect = 6e-65, Method: Compositional matrix adjust.
 Identities = 179/585 (30%), Positives = 280/585 (47%), Gaps = 82/585 (14%)

Query 46 SCETYVTYISQSPNFLSLTSVSNIFDTSPLSIARASNLQHEEDKLIPGQVLLIPVTCGCT 105
 Sbjct 53 SCAYLIFRSQP-YSTVASISTLLGSDPSQLSINS-ETTSFPTNQLVLVNCSCS 110

Query 106 GNRSFANISYEINQGDSFYFVATLTYQNLNTNWAVMDLNPGLSQFTLPIGIQVVIPLFCK 165
 Sbjct 111 GDYFQANASYIVQSGNTPFLIANNTYQGLSTCQAIRN-EKGTRTVNIFAGETLTVPLRCA 169

Query 166 CPSKNQLDRGIKYLITHWQPNNDVNSFVNKLGLASPQDILENNYQG-NFTAASNLPVLI 224
 Sbjct 170 CP+KNQ D GI+YL+++ D VS + GA L N + N T +LI CPTKRNSDLGIRYLLSYLTVWGDTVSIAGVRFGADIGRALEANEISEKNPTIYPTTLLI 229

Query 225 PVTLLPDLIQS-----PSDGRKHRIGLPVIIGISLGCTILLVVVSAI 265
 Sbjct 230 P+ P Q+ SD ++ + V +G G L +V+ I PLKNPTSSQTVVPPPPASPPSPSPNSDKSANKTWIYVFVGAvggivltvlgiti 289

Query 266 LLVCVCCCLKMKS-----LNRSASSAETADKLLSGVSGYVSKPTMYETGA 309
 Sbjct 290 + + K LNR E LL V +Y IF FMLFRSKKQPGPII VSQSFEAHEKPLNRKLD--EEPQDLLESVYSISQSIKVNYED 347

Query 310 ILEATMNLSECKIGESVYKANIEGVLAVERKRFKEDVTEELKILQKVNHGNLKVLMGVSS 369
 Sbjct 348 + AT N S I SV++ I G A+K DV+E+ I L K+NH NL+L GV LKAATDNFSFSWIKGSVFRGLINGDFAAIKMMNGDVSKEIDLNLKINHSNLIRLSGVCF 407

Query 370 DNDGNCFVYYEYAENGSELLEFWAKSCSETNSRTSLTWCQRISIAVDVSMGLQYMHEHA 429
 Sbjct 408 -NDGHWYLYEYAANGPLSDWIYV---SSNEGKFKWTQRIQIATDVATGLNLYLHSFT 461

Query 430 -YPRIVHRDITSSNILLDSNFKAKIANFSMARTFTNP----- 465
 Sbjct 462 YP VH+DI SSNILLD + +AKIANFS+AR+ P NYPH-VHKDIKSSNILLDKDLRAKIANFSLARSTDGPEGEFALTRHIVGKGYMAPEYLE 520

Query 466 ---MMSKIDVFAFGVVLIELLTGRK--AMTTKENGEVVMLWDIWK-IFDQEENREERLR 519
 Sbjct 521 + +K+DV+AFG++ E++TG++ A+ +EN E+ D+ + +E EE L NGIITCKLDVYAFGILTEIMTKEVAALYREENREL---SDVLNGVLSEEGGLEESLS 576

Query 520 KWMDPKLDNYYPIDYALSLASLAVNCTADKSLSRPTIAEIVLSSL 564
 Sbjct 577 + +DP + YP A+ + L +C RP + EIV SLS QLIDPSMQGNYPSGLAVLVMVRLLIDSCLNKNPAGRPMDEIVQSL 621

>**gb|ABQ59612.1|** LYK4 [Glycine max]
 Length=633

Score = 253 bits (645), Expect = 8e-65, Method: Compositional matrix adjust.
 Identities = 191/629 (30%), Positives = 322/629 (51%), Gaps = 77/629 (12%)

Query 7 SLTGLAQIYLVYVLMFFTCIEAQSQQTNGTNFSCPSNSPPSCETYVTYISQSPNFLSLTSV 66
 Sbjct 20 SL LG Q Y+ L C + + + + +C + + SC+Y+T+ SQ P + S+ ++ SLILGQQP-YIGLGTVC-PRRGNKNSIRGYTC-NGANHSCQSYLTFRSQ-PIYNSVKTI 75

Query 67 SNIFDTSPLSIARASNLQHEEDKLIPGQVLLIPVTCGCTGNRSFANISYEINQGDSFYFV 126
 S + + P + + + D +++++PV C C G N SYE + + + +
 Sbjct 76 STILLGSDPSQLAKINSVSMN-DTFETNKLVIVPVNCSCAGEYYQTNTSYEFHNSETYFLI 134

Query 127 ATTLYQNLTNWHAVMDLNPLGSQFTLPIGIQVVIPLFCCKCPSKNQLDRGIKYLITHVWQP 186
 A + + LT A+ N + P G + + + PL C CP+KNQ ++GI+YL+ + +
 Sbjct 135 ANNTFEGLTTCQALENQHNPANI-YP-GRRLLVPLRCACPTKRNQTEKGIRYLLSYLVNW 192

Query 187 NDNVSFVSNKLGASPQDILSENNYQONFTAASNLP--VLIPVTLLPDLIQSPPSDGRKHR 243
 D+VSF+S K G + L N T A+ P +L+P+ P Q+ S R+
 Sbjct 193 GDSVSIKEFGVNFMTTLEANTL--TLTQATIYPFTTILVPLHDKPSSSQTVSPTRRTP 250

Query 244 IGLPVIIGISLGCT----LLVVVSAILLVCVCC-----LKMKSLN 279
 P S T + VVV AI L+ V C + KS
 Sbjct 251 PPSPSSDHSSNKTWVYVVGVVVGAIALISLVCIAVIFTRYRKRNKKDDSVVVGSKSFE 310

Query 280 RSASSAETA--DKLLSGVSGYVSVKPTMYETGAILEATMNLSEQCKIGESVYKANIEGKVL 337
 E +KL +SG +Y + AT N S I SYV+ I G +
 Sbjct 311 AIEEKPEVKVNEKLSEIIISGIAQSFKVYINFEELQRATDNFSPPSWIKGSVYRGVINGDLA 370

Query 338 AVKFKFEDVTEKILKQVNHGNLKVLMGVSSNDGNCFVYEAENGSLLEEWLFAKSCS 397
 A+KR + DV+E++IL K+NH N++L GVS ++G ++VYEA NG L EW++ + +
 Sbjct 371 AIKRIEGDVSKEIEILNKHNSNVIRLSGVSF-HEGGWYLVYEAANGLSEWIYFHNVN 429

Query 398 ETNSNRTSLTWCORISIAVDVSMGLQYMHEAYPRIVHRDITSSNILLDSNFKA KIANFS 457
 L+W QR+ IA+DV+ GL Y+H P +H+DI SSNILLD +F+ K+ N S
 Sbjct 430 ----GKFLSWTQRMQIALDVA TGLYHSFTSPPHIHKDINSSNILLGDFRGKVTNLS 484

Query 458 MARTFT-----NPMMS-KIDVFAGVVLIELLTGRK--AM 489
 +AR N + +S K+DV+A FGV+++E++TG++ A+
 Sbjct 485 LARCLEGGDDQLPATRHIVGTRGYMAPEYYLENLVSTKLDVYAFGVIMLEMVTGKEVAI 544

Query 490 TTKENGEVVMLWKDIWKFIDQEENREERLRKWMDPKLDNYYPIDYALSLASLAVNCTADK 549
 T++ ++ + I EE+ +E L+++DP L P++ A+ + + NC
 Sbjct 545 LTEDETKLSHVLSGILG---EESKGKEMLKFEVDPDSLGENCPLELAMFVIEMIDNCIKTD 600

Query 550 SLSRPTIAEIVLSSLTQPSPLERSL 578
 SRP++ EIV S+S T S + ERS+
 Sbjct 601 PASRPSVHEIVQSMS-RTLKSSLWERSM 628

>ref|XP_002327712.1| predicted protein [Populus trichocarpa]

gb|EEE75190.1| predicted protein [Populus trichocarpa]

Length=630

Gene ID: 7464252 POPTRDRAFT_796841 | hypothetical protein [Populus trichocarpa] (10 or fewer PubMed links)

Score = 249 bits (635), Expect = 9e-64, Method: Compositional matrix adjust.
 Identities = 178/583 (30%), Positives = 290/583 (49%), Gaps = 80/583 (13%)

Query 46 SCETYVTYISQSPNFLSLTSVSNIFDTSPLSIARASNLQHEEDKLIPGQVLLIPVTCGCT 105
 SC+ Y+ + SQ P + ++ S+S + + P + + +++ E Q+ + + PV C C+
 Sbjct 42 SCQAYLIFRSQP-YNTVASISTLGSQDPSQLSEVNSTS-ETTSFPSNQLVIVPVNCSCS 99

Query 106 GNRSFANISYEINQGDSFYFVATLTYQNLTNWHAVMDLNPLGSQFTLPIGIQVVIPLFC 165
 G S AN SY + D+ + +A YQ L+ A+ + + L G + +PL C
 Sbjct 100 GEYSQANASYIVQPNNDTLFLIANNTYQGLSTCQALQNQKTTTRDDILS-GETLTVPRLCA 158

Query 166 CPSKNQLDRGKYLITHVWPQPNNDVSVSNKLGASPQDILSENNY-GONFTAASNLPVLI 224
 CP+KNQ D GI+Y++ + S + GA+ L N QN T +LI
 Sbjct 159 CPTKRNSQDLGIRYLLSLSYLTVPGDDVPAISEQFGAATGRTLEANGLPEQNPPTIFPFLLI 218

Query 225 PVTLLPDLIQS-----PSDGRKHRIGLPIVIGISLGCTLLVVSAILL 267
 P+ P Q+ + + + L V++G+ G L +V+ I+
 Sbjct 219 PLQSTPTSSQTVWPVPPPPASSSSPPSPNPEKSSKKTWLYVVGVGGIALTIVIGTIIF 278

Query 268 VCVCLKMKS-----LNRSASSAETADKLLSGVSGYVSKPTMYETGAIL 311
 + K LN+ E + + +S +Y+ +
 Sbjct 279 FMLSRKSKKQPGPVIESQSFEAHEKPLNKLD--EESQEFFFESISAIAQSIIKVKFEDLK 336

Query 312 EATMNLSEQCKIGESVYKANIEGKVLAVKRFKEDVTEELKILQKVNHNGLVKLMGVSSDN 371
 AT N S C I SYV+ I G A+K+ DV++E++L K+NH NL++L GV N
 Sbjct 337 AATDNFSPSCWIKGSVYGRILINGDFAAIKCMNGDVSKEIELINKINHNSNLIRLSGVCF-N 395

Query 372 DGNCFVYVYEAENGSLLEEWLFAKSCSETSNSRTSLTWCORISIAVDVSMGLQYMHEHA-Y 430
 DG+ ++VYEA +G L +W++ +S N L W +RI IA DV+ GL Y+H Y
 Sbjct 396 DGHWYLVYEAASQQLSDWIYDRS---NEGKFLNWTKRIQIASDVATGLNYLHSFTNY 450

Query 431 PRIVHRDITSSNILLDSNFKA KIANFSMART-----FTNP----- 465
 P VH+DI SSSNLLD+ +AKIANFS+AR+ + P
 Sbjct 451 PH-VHKDIKSSNILLDSDLRAKIANFSIARSTGDQDEFVLT R HIVGTRGYMAPEYLENG 509

Query 466 -MMSKIDVFAFGVVLIELLTGRK--AMTTKENGEVVMLWKDIW-IFDQEENREERLRKW 521
 + SK+DV+AFG++ +E+TG++ A+ ++E+ + D+ + + +EE L++
 Sbjct 510 VVSSKLDVYAFGILTLEIITGKEVAALHSEESRNL---SDVLNGALSEVDGQEEALKL 565

Query 522 MDPKLNDNYYPIDYALSLASLAVNCTADKSLSRPTIAEIVLSSL 564
 +DP L YP A+ + L +C RPT+ EIV SLS
 Sbjct 566 IDPSLHENYPSGLAVLVLVRIDLSDCLNKNPGDRPTMDEIVQSL 608

>ref|NP_001058110.1| Os06g0625200 [Oryza sativa Japonica Group]

dbj|BAD35689.1| receptor protein kinase-like [Oryza sativa Japonica Group]

dbj|BAD37734.1| receptor protein kinase-like [Oryza sativa Japonica Group]

dbj|BAF20024.1| Os06g0625200 [Oryza sativa Japonica Group]

gb|EAZ37689.1| hypothetical protein OsJ_22029 [Oryza sativa Japonica Group]

Length=630

Gene ID: 4341567 Os06g0625200 | Os06g0625200 [Oryza sativa Japonica Group] (10 or fewer PubMed links)

Score = 242 bits (618), Expect = 8e-62, Method: Compositional matrix adjust.

Identities = 171/568 (30%), Positives = 291/568 (51%), Gaps = 66/568 (11%)

Query 46	SCETYVTYISQSPNFSLSLTSVSNIFDTSPLSIARASNLQHEEDKLIPGQVLLIPVTCGCT	105
SC	Y+T+ S P SV+ + +P ++A A++ + Q+LL+PV C C	
Sbjct 56	SCATYLTFRSDPP-----LSVAYLLNATPSAVAAANSPLAVSPVDTQLLLVEVPCSC-	109
Query 106	GNRSFA----NISYEINQGDSFYFVATTLYQNLTNWHAVMDLNPGLSQFTLPIGIQVVIP	161
NR+	N +Y I + D+F+ +A +Q LT + +++ NP + I + +P	
Sbjct 110	-NRATGYYQHNTTYAIQELDTFFLIANNTFQGLTTYQSIIANNPASEAMSPVINGPLAVP	168
Query 162	LFCKCPSKNQLDRGIKYLTHWQPNNDNSFVSNKLGASPQDILSENNYQGNFTAASNLP	221
L C CPS	I L+T+V Q DNv+ ++ + ++ D+L+ N +	
Sbjct 169	LCACAPSATTGR--INNLITYVVQEGDNVTSIARRFNSTHGDLAANTLLVPLVHPPHSR	226
Query 222	VLIPTVLLPDLIQSPSDGRKHRI----GLPVIIGISLGCTL--LVVSAILLVCVCL	273
V++ T +	+P + K + GL +GI +GC + V A+ L+	
Sbjct 227	VVILANTITTS--TPPESQKFVYSSPCNSNGLLAQGLGIVGCGVSAAWAVLAVFLWRRRR	284
Query 274	KMKSLNRSASSAETADKLLSGVSGYVSKPTMYETGAILEATMMLSEQCKI--GESVYKAN	331
+	+ S + ET L++ V G V Y I AT +E+ ++ G SV+A	
Sbjct 285	RRPGDSSGMARE--PLVAAVRGAVETLAAYSYADIETATAGFAEERRVAAGSSVYRAV	342
Query 332	IEGKVLAVKRFK---EDVTEELKILQKVNHGNILKLMGVSSNDGNCFVVYEAENGSL	388
I G+ AVKR	+DV E+ +VNH LV+L G+ ++ D+ ++V E+AENG+L	
Sbjct 343	INGEAFAVKRVAAAGGDDVRGEVDVLGRVNHSGLVRLRGLCAND-DTYLVLEFAENGALS	401
Query 389	EWLFAKSCSETNSRTSLLTWCQRISIAVDVSMGLQYMHEAYPRIVHRDITSSNILLDSN	448
EWL S + R L W QR+ +A+DV+ GL Y+H P VH++ S N+LLD+N		
Sbjct 402	EWLHPGSAAACL--RRVLGWQKQRLVALDVAGGLNLYHHFTNPPVHKNLNSCNVLLDAN	459
Query 449	FKAKIANFSMA-----RTFTNP-----MMSKIDVFAGV	477
+AK+++ A	+ P + K+DVF+FCV	
Sbjct 460	LRAKSSLGFARAVAVAVAAGDDDSIALMTHHVVGTHGYLAPEYLEHGLISPKLDVFSFGV	519
Query 478	VLIELLTGR-KAMTTKENGEVVMLWKDIWIKFIDQEEENREERLRKWMDPKLDNNYPIDYAL	536
+ELL+G+ A T ++G+ ++LW+ D + LR +MDP+L +YPI A		
Sbjct 520	IQLLELLSGKTAACFTDDGQNMLLWQAADGLVDD-GDAGFWKLRAFMDPQLQGHPIGVAS	578
Query 537	SLASLAVNCTADKSLSRPTIAEIVLSSL	564
++A+LAV C A + +RP++ E+ ++LS		
Sbjct 579	AVAALAVRCVAREPRARPMSMEEVFVTL	606

>ref|XP_002307830.1| predicted protein [Populus trichocarpa]

gb|EEE94826.1| predicted protein [Populus trichocarpa]

Length=659

GENE ID: 7479122 POPTRDRAFT_862283 | hypothetical protein [Populus trichocarpa] (10 or fewer PubMed links)

Score = 239 bits (611), Expect = 7e-61, Method: Compositional matrix adjust.
Identities = 170/591 (28%), Positives = 290/591 (49%), Gaps = 86/591 (14%)

Query 46	SCETYVTYISQSP-NFLSLTSVSNIFDTSPLSIARASNLQHEEDKLIPGQVLLIPVTCGCT	104
SC++Y+T+ S P N L + S IA +NL + + ++PV C C		
Sbjct 58	SCQSYLTFRSMPYNSPVLIAVLLGVPQSATRIASINNLSSDTATIPTNTQVVVPVCSC	117
Query 105	TGNRSFA-NISYEI-NQGDSFYFVATTLYQNLTNWHAVMDLNPGLSQFTLPIGIQVVIPL	162
+ + N +Y++ ++ ++++ VA YQ LT ++M NP L +G+ + IPL		
Sbjct 118	YARQYYQHNSTTYQLDKSETYFSVANNTYQGLTCQSLMSQNP-YGDRNLSLGLTLQIPL	176
Query 163	FCKCPSKNQLDRGIKYLTHWQPNNDNSFVSNKLGASPQDILSENNYQGNFTAASNLPV	222
C CP+ NQ GI +LT++ D+S ++ G Q +L N + P+		
Sbjct 177	RCACPTSNQNAGSINHLLTLYMVWGDSISSIAQLGFDVKQRVLANKLSSNNIIFPFTPI	236
Query 223	LIPVTLVPDLI-----QSPS---DGRKHRIGLPVIIGISLGCTLVVVSA	264
L+P+ P I Q+P+ H+ + +G+ +G L+++ A		
Sbjct 237	LVP LPTEPTKIEQPSAAPPPAAPSPQTNPVSVGGSSDHK---ALYVGVGIGAAFLILLFA	293
Query 265	ILLVCVCCILKMKSLNRSASSAETADKLLSGVSGYVSKP-----T	303
K + + S+E + L S + + P T		
Sbjct 294	AFGFLFWHRKSRSQQPKVSTSE-PETLPSVSTDFTVLPVPSNNKWSWSLSSHADARYAIESLT	352
Query 304	MYETGAILEATMNLSEQCKIGESVYKANIEGKVLAVKRFKEDVTEELKILQKVNHGNLVK	363
+Y+ + AT ++ I SVY+ + +G AVK K DV+ E+ IL+ +NH N+++		
Sbjct 353	VYKYEDLQVATGYFAQANLIKGSVYRGSGFKDTAAVKKVVKGDVSSEINILKMINHSNVIR	412
Query 364	LMGVSSDNDNCFVYVEYAENGSLLEEWLFAKSCSETSNSRTSLLTWCQRISIAVDVSMGLQ	423
L G + +GN ++VYEA+NGSL +WL + +N L W QR+ IA DV+ L		
Sbjct 413	LSGFCL-HEGNTLYVVEYADNGSLTDWL-----HSNNIYRILAWKQRVRIAYDVADALN	465
Query 424	YMHEAYPRIVHRDITSSNILLDSNFKA KIANFSMARTFTNP-----	465
Y+H + P +H++ +SNILLD+N +AK+ANF +ART N		
Sbjct 466	YLHNYTNPSYIHKNLKTSNILLDANLRAKVANGFLARTLENGDGGQLQLTRHVGQTQGYL	525
Query 466	-----MMSKIDVFAGVVLIELLTGRKAMTT--KENGEVVMLWKDIWIKFIDQEEEN	513
+ K+DVFAGVV++ELL+G+A T K G+ +L I ++ +N		
Sbjct 526	APEYIENGVITPKL DVFAFGVVMLELLSGKEAAATAIDKIAGD-DLLSVMIMRVL-EGDN	583
Query 514	REERLRKWMDPKLDNNYPIDYALSLASLAVNCTADKSLSRPTIAEIVLSSL	564
E+L ++DP L + YP+D A S+A LA +C +RP++ ++ + LS		
Sbjct 584	VREKLSAFLDPCLRDEYPLDLA FMSAQLAKSCVEHDLNTRPSMPQVFMMMS	634

>emb|CAO02961.1| LysM-domain containing receptor-like kinase [Medicago truncatula var. truncatula]
Length=131

Score = 238 bits (606), Expect = 2e-60, Method: Composition-based stats.
Identities = 109/130 (83%), Positives = 120/130 (92%), Gaps = 0/130 (0%)

Query 411	RISIAVDSMGLQYMHEAYPRIVHRDITSSNILLDSNFKA KIANFSMARTFTNPMMMSKI	470
RI+IA+DV+ +GLQYMHEH YPRI+HRDIT+SNILL SNFKAKIANF MART TN MM KI		
Sbjct 1	RI TI AMDVAIGLQYMHEHTYPRIIHRDITTSNILLGSNFKA KIANFGMARTSTSNSMMPKI	60
Query 471	DVFAFGVVLIELLTGRKAMTTKENG EVVMLWKDIWKFIDQEEENREERLRKWM DPKLDNYY	530
DVFAFGVVLIELLTG+KAMTTKENG EVV+LWKD WKIFD E N REERLRKWM DPKLDNYY		

Sbjct 61 DVFAFGVVLIELLTGKKAMTTKENGEVVILWKDFWKIFDLEGNREERLRKWMDPKLESFY 120
 Query 531 PIDYALSLAS 540
 PID ALSLAS
 Sbjct 121 PIDNALSLAS 130

>ref|XP_002509540.1| ATP binding protein, putative [Ricinus communis]
 gb|EEF50927.1| ATP binding protein, putative [Ricinus communis]
 Length=681

GENE ID: 8271475 RCOM_1677900 | ATP binding protein, putative [Ricinus communis]

Score = 236 bits (602), Expect = 7e-60, Method: Compositional matrix adjust.
 Identities = 192/638 (30%), Positives = 304/638 (47%), Gaps = 101/638 (15%)

Query 25 IEAQSQQTNGTNFSCPSN-SPPSETTYVTYISQSPNFSLTSVSNNIFDTSPLSIARASNL 83
 + + + + + C N S C+T+ +S + F SL++S + IA A+ 88
 Sbjct 30 LSCETTSPDASGYRCNINGSQDHCKTFAI-LSTNSYFSSLSNLNFYLGFNRFVIAEANGF 88

Query 84 QHEEDKLIPGQVLLIPVTCGCTGNRSFANISYEINQGDSFYFVATTLYQNLTNWHA VMDL 143
 + + L Q LLIP+ C C GN A ++ +G+FY +A +L + LT A+ +
 Sbjct 89 SADTEFLPKDQPILLIPIDCKCNGNFFRAEVTKTTIKGENFYGAESL-EGLTCKAIQEN 147

Query 144 NGPLSQFTLPIGIQVVIPLFCCKCP SKNQLDRGIKYLITHVWQPNDNVSFVSNKLGASPQD 203
 N G+S + L + + +PL C CPS +Q+ +L+++ D +S ++ K +P+
 Sbjct 148 NLGVSPWNLADKARLLVPLRCACPSSQVTLATRFLLLSYPVSEGDITISNIAIKFNTTPEA 207

Query 204 ILSENNNG-QNFTAASNLPV---LIPVTLPPDL--IQSPSDGRK--HRIGLPV----- 249
 I+S NN NF +P+ LIP+ P L + P + +PVI
 Sbjct 208 IISANNRSLANFKPENLVPPLASLLIPLNREPALGSLAKPREPNSPFRESSIPVINPHKK 267

Query 250 -----IGISLGCTLLVV---VSAIILVCVCLKMKSLNR-----SASSAETAD 289
 IG+ + T +VV V+A L+V + K ++L++ S S T++
 Sbjct 268 SKMWMIGVYIAVTGVVVGATIAIAFLIVQLKKKKQNLSDGDPELQQLSLSVRTTSE 327

Query 290 KLLS--GVSGYVSKPTM-----YETGAILEATMNLISEQCKIGESVYKANIEG 334
 K +S G + + Y + +AT + S I SVY + G
 Sbjct 328 KKVSFEQSQQDLDNQIIDTTPRNRKVLVENYTVEELRKATEDFSSSSLIDGSVYYGRLNG 387

Query 335 KVLAVKRFKFEDVTEELKILQKVN---HGNLVKLMGVSSDNDGNCFVVYEAENGSLLEW 390
 K LA+KR K + ++ N H N++L+G + F+V+YE+A+NGSL+ +W
 Sbjct 388 KNLAIKRTKSETISKIDFHSFQNATHHNPNIIRLLGTCLSEGSDFLVFEYAKNGSLKD 447

Query 391 L-----FAKCSSETNSRTSLTWCQRISIAVDVSMGLQYMHEHAYPRIVHRDITSS 441
 F SC LTW QR+ I +DV+ LQYMH P VHR++ S
 Sbjct 448 LHGLLAMKNQFIASC-----YCFLTWNQRLKICLDAVALQYMHIMNPSYVHRNVKSR 501

Query 442 NILDSNFKAKIANFSMARTF-----TNP-----MMSKIDVF 473
 NI LD F AKI NO MAR TNP + ID+F
 Sbjct 502 NIFLDEEFNAKIGNFGMARCIEGDTQNTIEIHSTNPSSWSLGYLAPEYIHQGIVSPCIDIF 561

Query 474 AFGVVLIELLTGRKAMTTKEN-GEVVMLWKDIWKFQDEENREERLRKWMKPDKLDNYPI 532
 AFGVVL+E+L+G++ +T +N GE L + K EN E LR+FMD L Y
 Sbjct 562 AFGVVLLEVLSGKRPITRDPDNKGEESNLLSEKMKSISSNENAGE-LREWMDNALGENYSF 620

Query 533 DYALSLASLAVNCTADKSLSRPTIAEVILSLSLTQPS 570
 D A++LA+IA +C ++ RP E+V LS L + S
 Sbjct 621 DTAVTLANLARSCVEEPSLRLPNAGELVEKLSRLVEES 658

>ref|NP_566689.2| CERK1 (CHITIN ELICITOR RECEPTOR KINASE 1); kinase/ receptor signaling protein/transmembrane receptor protein kinase [Arabidopsis thaliana]

 dbj|BAF92788.1| chitin elicitor receptor kinase 1 [Arabidopsis thaliana]
 Length=617

GENE ID: 821717 CERK1 | CERK1 (CHITIN ELICITOR RECEPTOR KINASE 1); kinase/receptor signaling protein/transmembrane receptor protein kinase [Arabidopsis thaliana] (10 or fewer PubMed links)

Score = 229 bits (583), Expect = 1e-57, Method: Compositional matrix adjust.
 Identities = 165/543 (30%), Positives = 273/543 (50%), Gaps = 77/543 (14%)

Query 81 SNLQHEEDKLIPGQVLLIPVTCGCT-GNRSFANISYEINQGDSFYFVATTLYQNLTNWHA 139
 S N++ ++D++ G +L+P C C G+ + N SY + Q D++ VA + Y NLT +
 Sbjct 71 SNIKDKDRIQMGSRVLPFPCECQPGDFLGHNFNSYVSRQEDTYERVAISNYANLTTMES 129

Query 140 VMDLNPGLSQFTLPIGIQVVIPLFCCKCP SKNQLDRGIKYLITHVWQPNDNVSFVSNKLG 199
 + NP +P+ + + C C ++ + +T+ +P D++S ++ G
 Sbjct 130 LQARNP-FPATNIPLSATLNVLVCNSCGDES-VSKDFGLFVTYPLRPEDSLSSIASRG 187

Query 200 SPQDILSENNYQGNFTAASN-----PVLI PVTLPLDIQSPSDGRKHRIGLPIIGISLGC 256
 S DIL N G NF + + P P S D DG +G VI GI +G
 Sbjct 188 S-ADILQRYNPGVNFNSNGNGIVYVPGDPNGAFPPFKSSKQDG---VGAGVIAGIVIGV 242

Query 257 TLVWVVAIILVCVCLKMKSLNRASSA-----ETADKLLSGVSG----- 297
 + +++ + +V K KS S SS+ ++ L SG G
 Sbjct 243 IVALLL-ILFIVYYAYRKNKSKGDSFSSSIPLSTKADHASSTSLSQSGGLGGAGVSPGIAA 301

Query 298 -YVSKPTMYETGAILEATMNLSQCKIGE---SVYKANIEGKVLA VKRKFEDVTE----- 348
 V K + + AT N + KIG+ +VY A + G+ A+K+ + ++
 Sbjct 302 ISVDKSVEFSLEELAKATDNFNLSFKIGQGGFGAVYYAELRGEKAIAKMDMEASKQFLA 361

Query 349 ELKILQKVNHNGLVLMGVSSDNDGNCFVVYEAENGSLLEEWLFAKSCSETSNSRTSLW 408
 ELK+L +V+H NLV+L+G + G+ F+VYEAENG+L + L + R L W
 Sbjct 362 ELKVLTRVHHVNLVRIGYCV--GSLFLVYEVYVENGLQHLHG-----SGREPLFW 412

Query 409 CQRISIAVDVSMGLQYMHEHAYPRIVHRDITSSNLLDSNFKAKIANFSMAR----- 460
 +R+ IA+D + GL+Y+HEH P VHRDI S+NIL+D F+AK+A+F + +
 Sbjct 413 TKRQVQIALDSARGLEYIHEHTVPPVYVHRDIKSANILIDQKFRAKVADFGLTKLTEVGGS 472

Query 461 -----TFTNPMMSKIDVFAFGVVLIELLTGRKAMTTKENGEVVMLWKDIW 506
 T + +K+DV+AFGVVL EL++ + A+ E V ++ +

Subjct	473	TRGAMGTGFGMAPETVYGEVSAKVDVYAFGVVLYELISAKGAVVKMT--EAVGEFRGLVG	530
Query	507	IFDQ---EENREERLRKWMDPKLDNYYPIDYALSLASLAVNCTADKSLSRPTIAEVILSL +F++ E ++EE LRK +DP+L + YP D +A L CT ++ RP++ IV++L	563
Subjct	531	VFEESFKETDKEEARLKIIDPRLGDSYPFDHSVYKMAELGKACTQENAQLRPSMRYIVVAL	590
Query	564	SLL 566	
		S L	
Subjct	591	STL 593	

ref XP_002300098.1 		predicted protein [Populus trichocarpa]
gb EEE84903.1 		predicted protein [Populus trichocarpa]
Length=680		
GENE ID: 7467712 POPTRRDRAFT_641782 hypothetical protein [Populus trichocarpa] (10 or fewer PubMed links)		
Score = 224 bits (572),	Expect = 2e-56,	Method: Compositional matrix adjust.
Identities = 192/629 (30%),	Positives = 296/629 (47%),	Gaps = 87/629 (13%)
Query 25	IEAQSSQQTNGTNFSCPNS-PPSCETYVTYISQSPNFSLTSVSNIFDTSPLSIARASNL	83
Sbjct 32	+ Q+ + + C SN C+T+ + S F SL++S IA + LSCQTTSPDASGYHCNSNGLQDQCKTFAI-LHTSSYFSSLSNLNFYIQLGLDRFVIAATNGF	90
Query 84	QHEEDKLIPGQVLLIPVTCGCTGNRSFANISYEINQGDSFYFVATTLYQNLTNWHAVMGL	143
Sbjct 91	+ L Q LLIP+ C C G A ++ +GSFY ++ +L + LT A+ + SANTEFLPKDQPLPPIIDCKCNGFFFQALVTKTITKGESYISKSL-EGLITCKAIREK	149
Query 144	NPGLSQFTLPIGIVQVVIPLFCCKCPKSQNLDRGIKYLITHVWQPNNDVSFVSNKLGASPFD	203
Sbjct 150	NPG+S L +Q+ +PL C CPS ++ + L+++ D +S ++ K +P+ NPGISPENLNKGKVQLQVPLRACPSSTEVLATRLLSYPVAGDTISNLAIFKNTPFEA	209
Query 204	IILSENNYG-QNFTAASNLPV---LIPVTLPPDL--IQSPSDGRKH--RIGLPVI-----	249
Sbjct 210	I S NN F S +P+ LIP+ P L P++ H LPVI ITSANNRSRLTTFKPTSLVPLTSSLIPLGKPTLGPLAKPEPNLHIPASSLVEVINPHKKR	269
Query 250	-----IGISLGCTLLVV----VSAILLVCVCCLKMKSLNRSA-----SSAETADK	290
Sbjct 270	IG+ + T VV ++A LV K + L++ A S T+DK SKMWRIGVYIAVTGAVVGVSIAIAAAFLVIQLKKKKVQLSKEADTELQQQLSLSVRTTSOK	329
Query 291	LLS-----GVSGYVSKPTMYETGAILE---ATMLNLSSEQCKVSYKANIEGKVL	337
Sbjct 330	+S ++ ET + E AT + + +I SVY + GK L KVSFDDSNQHFDQSITDTTPGKVFVETYTVEELKRATEDFNSSNQIEGSVYHGRLNGKL	389
Query 338	AVKRFKFEDVTE--ELKILILQKV--NHGNILVKLMGVSSDMDGNCFVYVEYAENGSLLEEWL--	391
Sbjct 390	A+KR + + EL + Q +H N+++++G + F+V+EYA+NGLS++WL AIKRVQPETISKVELGLFQDATHHPPNIIRVVGTCLESEGPDSDLVFEYAKNGSLKDWLHG	449
Query 392	-FAKCSSETNSRSTSILTWCQRISIAVDSMGLQYQMHEAYPRIVHRDITSSNILLDSNFK	450
Sbjct 450	A ++ LTW QR+ I +DV++ LQYMH +P VHR+I S NI LD F GLAMKNQFIASCYCFLTWNQRQLKICLDVAVALQYMHHIMHPSPVYHNRNIKSRNIFLDEEFN	509
Query 451	AKIANFSMARTF-----TNP-----MMSKIDVFAGFVGVLIELL	483
Sbjct 510	AKI NF MA TNP + S D+F+FGVVL+E+L AKIGNFGMAGCVEDDTKEPDFNSTNPASWLSLGYLAPEAHQGVVSSSTDIFSGVVIMEVL	569
Query 484	TGRKAMTT-KENGE-VVMLWKDIWIKIFDQEENREERLRKWMDPKLKDNYYPIDYALSLASL	541
Sbjct 570	+G+ +T +NGE + L K I I EN +E LR+W+D + Y D A +LA++ SGQTPITRPNDNGEGSIWLSKKIKSIL-LSENADE-LREWIDSAMGENYSFDEAATLANI	627
Query 542	AVNCTADKSLSLRPTIAEVILSLSLLTQPS 570	
Sbjct 628	A CT + RPT EIV L L + S ARACTEEDPSLRPTSGEIVEKLLRLVEES 656	

>**ref|XP_002263070.1|**  PREDICTED: hypothetical protein [Vitis vinifera]
Length=675

Gene ID: 100264694 LOC100264694 hypothetical protein LOC100264694 [Vitis vinifera] (10 or fewer PubMed links)											
Score = 224 bits (571), Expect = 3e-56, Method: Compositional matrix adjust Identities = 182/667 (27%), Positives = 303/667 (45%), Gaps = 91/667 (13%)											
Query	1	MAVFFVSLTLGAQILYVVLMLFTC	---	IEAQSQQTNGTNFSCPSN	-SPPSCSETYVTYIS	55					
Sbjct	1	MAA	L A	L + + +	T	+ + +	+ + C	N S	C T +	+ +	
Query	56	QSPNFLSLSLTSVSNIDFTSPLSIARASNLQHEEDKLI	P	GQVLLIPVTCGCTGNRSFANSIY	S	+	SL	++ S	IA	A +	115
Sbjct	61	NS-YYSSLNFNLSFYLGIDRFLIAEANGFSADTELLP	N	YLNPLLLPIECKCKAGFFQAELTK	Y	S	Y	S	A +	L	119
Query	116	EINQGDSFSYFVATTLYQNLTNWAVMDLNPGSQFTLPI	G	IGIQVVIPLFKCPSKNQLDRG	+G+S+	F	+A	+ L	LT	A +	175
Sbjct	120	TTIEGESFFGIAESL-EGLITCKKAIRRNPSIQP	G	WGLADKVRLLPIPLRCAPCSSELIQE	+	G	+ +	+ NP	+ L	+++ I	178
Query	176	IKYLITHWWQPNNDNVSVNKNLKGASPQDILSEN	K	YIPL	+	L	+	I+S	NN	G	231
Sbjct	179	TKLILSYVPSEGDTVPSLAFKFNTTSEAIISANRNRSGATLRLGS	L	PLPVSSLLIPLRDKPT	+	L	++ +	I	D V	S	238
Query	232	LIQSPSPDGRKRHIGLPV	L	-----	S P+	R +	+ GLP	-----	I	IGISLGC	267
Sbjct	239	L-GSPAKPREPNLGLPATSI	G	-----	P	V	+	I	+	LLVVVSAILL-	297
Query	268	-----VCVCLKMKMSLNRSASSAETADKL	-----	LSGVGSVSKPTMYETGAILE	-----	-----	-----	-----	-----	-----	312
Sbjct	298	WKRKKQNAKMGDVELQQLGLS	+	ET + LE	+	L	+++ +	S E +	+	-----	357
Query	313	---ATMNLSEQCKIGEVSYKANIEGKVLA	AT	-----	RVKFEDVTE	+	+	I	SV +	+ GK	365
Sbjct	358	LRKATEDDFNSSNLIEGSV	+	-----	LA+K	+	E +	+	LA	+ H N + + L	417
Query	366	GVSSNDGNCFVVYEAENGSL	G	-----	EWEL--	+	+	+	+EY+A+NGS	+WL	422
Sbjct	418	GTCLNEGPDSY	G	-----	LTWQR	+	++	Y	AKNGSLKDWHGLAMKSQFI	ASCYCFL	477
										WTQNRLRICLDVAMAL	

Select All Get selected sequences Distance tree of results Multiple alignment

APPENDIX B

BLAST**Basic Local Alignment Search Tool**

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[Edit and Resubmit Save Search Strategies Documented](#)**SEQID48 (598 letters)**Results for: lcl|33458 SEQID48(598aa)

Your BLAST job specified more than one input sequence. This box lets you choose which input sequence to show BLAST results for.

 lcl|33458
lcl|33458**Description**

SEQID48

Molecule type

amino acid

Query Length

598

Database Name

nr

Description

All non-redundant GenBank CDS translations+PDB+SwissProt+PIR+PRF excluding environmental samples from WGS projects

ProgramBLASTP 2.2.24+ [Citation](#)[Reference](#)

Stephen F. Altschul, Thomas L. Madden, Alejandro A. Schäffer, Jinghui Zhang, Zheng Zhang, Webb Miller, and David J. Lipman (1997), "Gapped BLAST and PSI-BLAST: a new generation of protein database search programs", Nucleic Acids Res. 25:3389-3402.

[Reference - compositional score matrix adjustment](#)

Stephen F. Altschul, John C. Wootton, E. Michael Gertz, Richa Agarwala, Aleksandr Morgulis, Alejandro A. Schäffer, and Yi-Kuo Yu (2005) "Protein database searches using compositionally adjusted substitution matrices", FEBS J. 272:5101-5109.

Other reports: [Search Summary](#) ([Taxonomy report](#)) ([Distance list of results](#)) ([Multiple alignment](#))[Search Parameters](#)**Search parameter name** **Search parameter value**

Program	blastp
Word size	3
Expect value	10
Hitlist size	100
Gapcosts	11,1
Matrix	BLOSUM62
Filter string	F
Genetic Code	1
Window Size	40
Threshold	11
Composition-based stats	2

Database

Database parameter name **Database parameter value**

Posted date	Sep 26, 2010 5:43 PM
Number of letters	4,071,357,309
Number of sequences	11,921,515
Entrez query	none

Karlin-Altschul statistics

Params **Ungapped** **Gapped**

Lambda	0.318422	0.267
K	0.132723	0.041
H	0.387288	0.14

Results Statistics

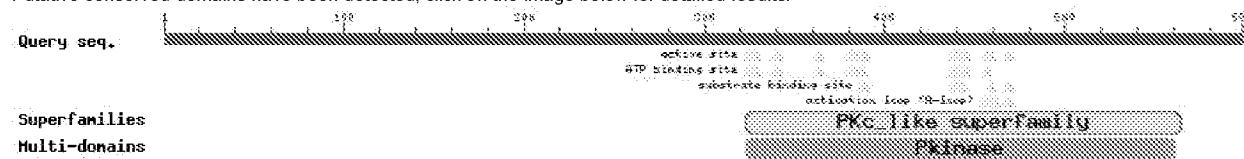
Results Statistics parameter name **Results Statistics parameter value**

Length adjustment	144
Effective length of query	454
Effective length of database	2354659149
Effective search space	1069015253646
Effective search space used	1069015253646

Graphic Summary

Show Conserved Domains

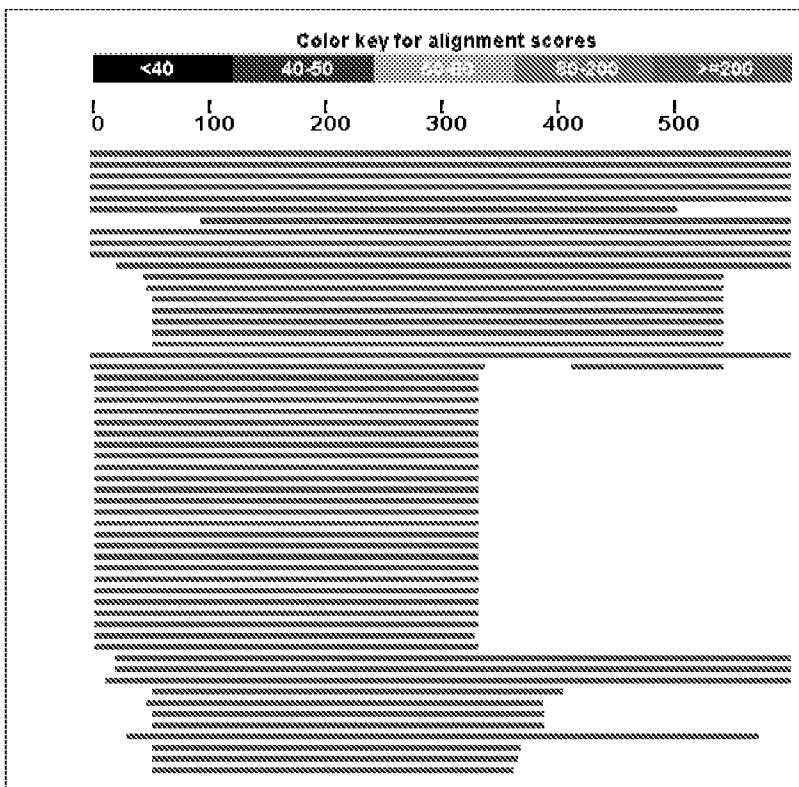
Putative conserved domains have been detected, click on the image below for detailed results.



Distribution of 102 Blast Hits on the Query Sequence

[?]

An overview of the database sequences aligned to the query sequence is shown. The score of each alignment is indicated by one of five different colors, which divides the range of scores into five groups. Multiple alignments on the same database sequence are connected by a striped line. Mousing over a hit sequence causes the definition and score to be shown in the window at the top, clicking on a hit sequence takes the user to the associated alignments. New: This graphic is an overview of database sequences aligned to the query sequence. Alignments are color-coded by score, within one of five score ranges. Multiple alignments on the same database sequence are connected by a dashed line. Mousing over an alignment shows the alignment definition and score in the box at the top. Clicking an alignment displays the alignment detail.



Descriptions

Legend for links to other resources: UniGene GEO Gene Structure Map Viewer PubChem BioAssay
Sequences producing significant alignments:

Accession	Description	Max score	Total score	Query coverage	E value	Links
ABQ098809..1	NFR5a [Glycine max] >gb ADJ19105.1 Nod-factor receptor 5A [Glycine max] >gb ADJ19108.1 Nod-factor receptor 5A [Glycine max]	1235	1235	100%	0.0	
ADJ19108..1	Nod-factor receptor 5A [Glycine max]	1233	1233	100%	0.0	
ADJ19107..1	Nod-factor receptor 5A [Glycine max]	1231	1231	100%	0.0	
ADJ19106..1	Nod-factor receptor 5B [Glycine max]	1106	1106	100%	0.0	
ADJ19105..1	Nod-factor receptor 5B [Glycine max]	1103	1103	100%	0.0	
ADQ098810..1	truncated Nod-factor receptor 5A [Glycine max]	1037	1037	83%	0.0	
ABQ098813..1	NFR5b [Glycine max]	957	957	84%	0.0	
CAE029303..1	SYM10 protein [Pisum sativum] >emb CAE02594.1 SYM10 protein [Pisum sativum]	899	899	100%	0.0	
CAE029301..1	SYM10 protein [Pisum sativum] >emb CAE02596.1 SYM10 protein [Pisum sativum] >gb ADB45277.1 Nod factor recognition protein [Pisum sativum]	895	895	100%	0.0	
CAE029307..1	Nod-factor receptor 5 [Lotus japonicus] >emb CAE02598.1 Nod-factor receptor 5 [Lotus japonicus]	875	875	100%	0.0	
ABF09224..1	Nod factor perception protein [Medicago truncatula]	864	864	96%	0.0	
CAO02936..1	LysM-domain containing receptor-like kinase [Medicago truncatula var. truncatula]	761	761	82%	0.0	
CAO02935..1	LysM-domain containing receptor-like kinase [Medicago truncatula var. truncatula]	754	754	82%	0.0	
CAO02933..1	LysM-domain containing receptor-like kinase [Medicago truncatula var. truncatula] >emb CAO02934.1 LysM-domain containing receptor-like kinase [Medicago truncatula var. truncatula] >emb CAO02935.1 LysM-domain containing receptor-like kinase [Medicago truncatula var. truncatula] >emb CAO02938.1 LysM-domain containing receptor-like kinase [Medicago truncatula var. truncatula] >emb CAO02939.1 LysM-domain containing receptor-like kinase [Medicago truncatula var. truncatula] >emb CAO02952.1 LysM-domain containing receptor-like kinase [Medicago truncatula var. longilobata] >emb CAO02955.1 LysM-domain containing receptor-like kinase [Medicago truncatula var. truncatula] >emb CAO02957.1 LysM-domain containing receptor-like kinase [Medicago truncatula var. truncatula] >emb CAO02959.1 LysM-domain containing receptor-like kinase [Medicago truncatula var. truncatula] >emb CAO02967.1 LysM-domain containing receptor-like kinase [Medicago truncatula var. truncatula] >emb CAO02971.1 LysM-domain containing receptor-like kinase [Medicago truncatula var. truncatula] >emb CAO02972.1 LysM-domain containing receptor-like kinase [Medicago truncatula var. truncatula] >emb CAO02973.1 LysM-domain containing receptor-like kinase [Medicago truncatula var. truncatula]	747	747	81%	0.0	
CAO02931..1	LysM-domain containing receptor-like kinase [Medicago truncatula var. truncatula]	745	745	81%	0.0	
CAO02930..1	LysM-domain containing receptor-like kinase [Medicago truncatula var. truncatula]	745	745	81%	0.0	
CAO02929..1	LysM-domain containing receptor-like kinase [Medicago truncatula var. truncatula] >emb CAO02970.1 LysM-domain containing receptor-like kinase [Medicago truncatula var. truncatula]	744	744	81%	0.0	
CAO02928..1	LysM-domain containing receptor-like kinase [Medicago tornata]	741	741	81%	0.0	
BAI79285..1	LysM type receptor kinase [Lotus japonicus] >dbj BAI79285.1 LysM type receptor kinase [Lotus japonicus]	704	704	100%	0.0	
AQJ19109..1	truncated Nod-factor receptor 5A [Glycine max]	695	695	56%	0.0	
BAG85149..1	Nod factor receptor protein [Glycine soja] >dbj BAG85149.1 Nod factor receptor protein [Glycine soja] >dbj BAG85156..1 Nod factor receptor protein [Glycine soja] >dbj BAG85159..1 Nod factor receptor protein [Glycine max] >dbj BAG85160..1 Nod factor receptor protein [Glycine max] >dbj BAG85161..1 Nod factor receptor protein [Glycine max] >dbj BAG85162..1 Nod factor receptor protein [Glycine max] >dbj BAG85165..1 Nod factor receptor protein [Glycine max] >dbj BAG85168..1 Nod factor receptor protein [Glycine max] >dbj BAG85171..1 Nod factor receptor protein [Glycine max] >dbj BAG85174..1 Nod factor receptor protein [Glycine max] >dbj BAG85177..1 Nod factor receptor protein [Glycine max] >dbj BAG85179..1 Nod factor receptor protein [Glycine max] >dbj BAG85180..1 Nod factor receptor protein [Glycine max]	675	675	54%	0.0	
BAG85148..1	Nod factor receptor protein [Glycine soja]	674	674	54%	0.0	
BAG85151..1	Nod factor receptor protein [Glycine soja]	673	673	54%	0.0	
BAG85178..1	Nod factor receptor protein [Glycine max]	673	673	54%	0.0	
BAG85167..1	Nod factor receptor protein [Glycine max]	673	673	54%	0.0	
BAG85184..1	Nod factor receptor protein [Glycine max]	673	673	54%	0.0	
BAG85179..1	Nod factor receptor protein [Glycine max]	672	672	54%	0.0	
BAG85166..1	Nod factor receptor protein [Glycine soja]	672	672	54%	0.0	
BAG85158..1	Nod factor receptor protein [Glycine max]	672	672	54%	0.0	
BAG85164..1	Nod factor receptor protein [Glycine soja] >dbj BAG85145.1 Nod factor receptor protein [Glycine soja]	672	672	54%	0.0	
BAG85142..1	Nod factor receptor protein [Glycine soja]	672	672	54%	0.0	
BAG85152..1	Nod factor receptor protein [Glycine soja]	672	672	54%	0.0	
BAG85175..1	Nod factor receptor protein [Glycine max]	672	672	54%	0.0	
BAG85172..1	Nod factor receptor protein [Glycine max]	671	671	54%	0.0	
BAG85157..1	Nod factor receptor protein [Glycine soja]	671	671	54%	0.0	
BAG85156..1	Nod factor receptor protein [Glycine soja]	671	671	54%	0.0	

BAQ885178.1	Nod factor receptor protein [Glycine max]	670	670	54%	0.0	
BAQ885183.1	Nod factor receptor protein [Glycine soja]	669	669	54%	0.0	
BAQ885185.1	Nod factor receptor protein [Glycine soja]	669	669	54%	0.0	
BAQ885183.1	Nod factor receptor protein [Glycine max]	669	669	54%	0.0	
BAQ885173.1	Nod factor receptor protein [Glycine max]	669	669	54%	0.0	
BAQ885184.1	Nod factor receptor protein [Glycine soja]	667	667	54%	0.0	
BAQ885189.1	Nod factor receptor protein [Glycine max]	665	665	54%	0.0	
BAQ885188.1	Nod factor receptor protein [Glycine max]	660	660	54%	0.0	
BAQ885187.1	Nod factor receptor protein [Glycine soja]	659	659	54%	0.0	
XP_0922889472.1	PREDICTED: hypothetical protein [Vitis vinifera] >emb CBI17584.3 unnamed protein product [Vitis vinifera]	654	654	96%	0.0	
XP_0922833280.1	serine-threonine protein kinase, plant-type, putative [Ricinus communis] >gb EEF29112.1 predicted protein [Populus trichocarpa] predicted protein [Populus trichocarpa] >gb EEE90648.1 predicted protein [Populus trichocarpa]	638	638	96%	0.0	
XP_0923310198.1	predicted protein [Populus trichocarpa] >gb EEE90648.1 predicted protein [Populus trichocarpa]	614	614	97%	1e-173	
CAQ028538.1	LysM-domain containing receptor-like kinase [Medicago truncatula var. truncatula]	499	499	58%	4e-139	
CAQ028538.1	LysM-domain containing receptor-like kinase [Medicago truncatula var. truncatula]	484	484	56%	2e-134	
CAQ028538.1	LysM-domain containing receptor-like kinase [Medicago truncatula var. truncatula]	481	481	56%	1e-133	
CAQ028538.1	LysM-domain containing receptor-like kinase [Medicago truncatula var. truncatula]	477	477	55%	2e-132	
XP_092488236.1	hypothetical protein SORBIDRAFT_01g042230 [Sorghum bicolor] >gb EER95234.1 hypothetical protein SORBIDRAFT_01g042230 [Sorghum bicolor]	441	441	90%	2e-121	
CAQ028538.1	LysM-domain containing receptor-like kinase [Medicago truncatula var. truncatula]	436	436	52%	6e-120	
CAQ028538.1	LysM-domain containing receptor-like kinase [Medicago truncatula var. truncatula] >emb CAO02968.1 LysM-domain containing receptor-like kinase [Medicago truncatula var. truncatula]	433	433	52%	4e-119	
CAQ028538.1	LysM-domain containing receptor-like kinase [Medicago truncatula var. truncatula]	427	427	51%	2e-117	
AAH19130.1	Putative protein kinase [Oryza sativa Japonica Group] >gb ABF94815.1 Protein kinase domain containing protein [Oryza sativa (japonica cultivar-group)] >gb EAZ26175.1 hypothetical protein OsJ_10042 [Oryza sativa Japonica Group]	426	426	93%	3e-117	
SAY89355.1	hypothetical protein OsJ_10648 [Oryza sativa Indica Group]	426	426	93%	6e-117	
CAQ028538.1	LysM-domain containing receptor-like kinase [Medicago truncatula var. truncatula]	422	422	51%	6e-116	
CAQ028538.1	LysM-domain containing receptor-like kinase [Medicago truncatula var. truncatula]	418	418	51%	9e-115	
XP_092283792.1	serine-threonine protein kinase, plant-type, putative [Ricinus communis] >gb EEF45192.1 serine-threonine protein kinase, plant-type, putative [Ricinus communis]	366	366	86%	5e-99	
XP_0922836970.1	PREDICTED: hypothetical protein [Vitis vinifera]	355	355	89%	8e-96	
AAV00791.1	SYM10-like protein [Galega orientalis]	351	351	40%	2e-94	
CSN28359.3	unnamed protein product [Vitis vinifera]	345	345	89%	1e-92	
ABR17893.1	unknown [Picea sitchensis]	343	343	76%	3e-92	
CAN93782.1	hypothetical protein [Vitis vinifera]	338	338	89%	1e-90	
XP_0922831853.1	predicted protein [Populus trichocarpa] >gb EEE89020.1 predicted protein [Populus trichocarpa]	324	324	76%	2e-86	
CAQ028538.1	LysM-domain containing receptor-like kinase [Medicago truncatula var. truncatula]	313	313	40%	6e-83	
SAY87582.1	hypothetical protein OsJ_08480 [Oryza sativa Indica Group]	313	313	88%	6e-83	
XP_091757824.1	predicted protein [Physcomitrella patens subsp. patens] >gb EDQ67338.1 predicted protein [Physcomitrella patens subsp. patens]	302	302	91%	8e-80	
BAI79275.1	LysM type receptor kinase [Lotus japonicus]	297	297	92%	2e-78	
XP_092283699.1	predicted protein [Populus trichocarpa] >gb EEE73651.1 predicted protein [Populus trichocarpa]	292	292	86%	8e-77	
XP_091753589.1	predicted protein [Physcomitrella patens subsp. patens] >gb EDQ51621.1 predicted protein [Physcomitrella patens subsp. patens]	291	291	90%	2e-76	
BAI79277.1	LysM type receptor kinase [Lotus japonicus] >dbj BAI79287.1 LysM type receptor kinase [Lotus japonicus]	286	286	87%	4e-75	
XP_092283756.1	kinase, putative [Ricinus communis] >gb EEF52943.1 kinase, putative [Ricinus communis]	283	283	85%	5e-74	
XP_092283889.1	BRASSINOSTEROID INSENSITIVE 1-associated receptor kinase 1 precursor, putative [Ricinus communis] >gb EEF39869.1 BRASSINOSTEROID INSENSITIVE 1-associated receptor kinase 1 precursor, putative [Ricinus communis]	280	280	86%	3e-73	
XP_092283895.1	hypothetical protein SELMODRAFT_11326 [Selaginella moellendorffii] >gb EFJ08078.1 hypothetical protein SELMODRAFT_11326 [Selaginella moellendorffii]	280	280	89%	3e-73	
XP_092283733.1	PREDICTED: hypothetical protein [Vitis vinifera]	280	280	91%	4e-73	
XP_092283443.1	hypothetical protein SELMODRAFT_11327 [Selaginella moellendorffii] >gb EFJ24716.1 hypothetical protein SELMODRAFT_11327 [Selaginella moellendorffii]	279	279	89%	7e-73	
CBH17883.3	unnamed protein product [Vitis vinifera]	277	551	88%	3e-72	
XP_092283333.1	serine-threonine protein kinase, plant-type, putative [Ricinus communis] >gb EEF52520.1 serine-threonine protein kinase, plant-type, putative [Ricinus communis]	276	276	86%	5e-72	
BAI79276.1	LysM type receptor kinase [Lotus japonicus]	276	276	91%	7e-72	
BAI79286.1	LysM type receptor kinase [Lotus japonicus]	276	276	91%	8e-72	
AEG399912.1	LYK4 [Glycine max]	270	270	96%	5e-70	
CBH17883.3	unnamed protein product [Vitis vinifera]	269	347	82%	1e-69	
XP_092283940.1	PREDICTED: hypothetical protein [Vitis vinifera]	268	268	88%	1e-69	
XP_092283379.1	serine-threonine protein kinase, plant-type, putative [Ricinus communis] >gb EEF29111.1	265	265	90%	2e-68	

	serine-threonine protein kinase, plant-type, putative [Ricinus communis]					
XP_0028833278.1	BRASSINOSTEROID INSENSITIVE 1-associated receptor kinase 1 precursor, putative [Ricinus communis] >gb EEF29110.1 BRASSINOSTEROID INSENSITIVE 1-associated receptor kinase 1 precursor, putative [Ricinus communis]	265	265	89%	2e-68	
XP_0022699498.1	PREDICTED: hypothetical protein [Vitis vinifera]	263	263	86%	4e-68	
XP_0023327712.1	predicted protein [Populus trichocarpa] >gb EEE75190.1 predicted protein [Populus trichocarpa]	258	258	86%	2e-66	
XP_002319777.1	predicted protein [Populus trichocarpa] >gb EEE91227.1 predicted protein [Populus trichocarpa]	254	254	86%	2e-65	
XP_0022381886.1	PREDICTED: hypothetical protein [Vitis vinifera]	253	253	86%	4e-65	
XP_0026095468.1	ATP binding protein, putative [Ricinus communis] >gb EEF50927.1 ATP binding protein, putative [Ricinus communis]	253	253	88%	4e-65	
NP_0010558115.1	Os06g0625200 [Oryza sativa Japonica Group] >dbj BAD35689.1 receptor protein kinase-like [Oryza sativa Japonica Group] >dbj BAD37734.1 receptor protein kinase-like [Oryza sativa Japonica Group] >dbj BAF2024.1 Os06g0625200 [Oryza sativa Japonica Group] >gb EAZ37689.1 hypothetical protein OsJ_22029 [Oryza sativa Japonica Group]	251	251	86%	3e-64	
XP_003387839.1	predicted protein [Populus trichocarpa] >gb EEE94826.1 predicted protein [Populus trichocarpa]	248	248	86%	2e-63	
CAQ82881.1	LysM-domain containing receptor-like kinase [Medicago truncatula var. truncatula]	240	240	21%	4e-61	
XP_002300093.1	predicted protein [Populus trichocarpa] >gb EEE84903.1 predicted protein [Populus trichocarpa]	238	238	93%	2e-60	
NP_0009988.2	CERK1 (CHITIN ELICITOR RECEPTOR KINASE 1); kinase/receptor signaling protein/transmembrane receptor protein kinase [Arabidopsis thaliana] >dbj BAF92788.1 chitin elicitor receptor kinase 1 [Arabidopsis thaliana]	236	236	80%	8e-60	
CSIA00054.3	unnamed protein product [Vitis vinifera]	234	234	95%	2e-59	
XP_002263079.1	PREDICTED: hypothetical protein [Vitis vinifera]	233	233	95%	4e-59	

Alignments

Select All Get selected sequences Distance tree of results Multiple alignment

>gb ABQ59609.1	NFR5a [Glycine max]					
gb ADJ19105.1	Nod-factor receptor 5A [Glycine max]					
gb ADJ19108.1	Nod-factor receptor 5A [Glycine max]					
Length=598						
Score = 1235 bits (3196), Expect = 0.0, Method: Compositional matrix adjust.						
Identities = 598/598 (100%), Positives = 598/598 (100%), Gaps = 0/598 (0%)						
Query 1 MAVFFPFLPLHSQILCLVIMLFSTNIVAQSQQDNRTNFSCPSDSSPPSCETYVTYIAQSPN	60					
Sbjct 1 MAVFFPFLPLHSQILCLVIMLFSTNIVAQSQQDNRTNFSCPSDSSPPSCETYVTYIAQSPN	60					
Query 61 FLSLTNISNIFDTSPLSIARASNLEPMDDKLVKDQVLLVPVTCGCTGNRSFANISYEINQ	120					
Sbjct 61 FLSLTNISNIFDTSPLSIARASNLEPMDDKLVKDQVLLVPVTCGCTGNRSFANISYEINQ	120					
Query 121 GD SYFVATT SYENLTN RAVMDLNPV LSPN KLP IGI QV VFP LCK C P SKN Q LD KE I KY L	180					
Sbjct 121 GD SYFVATT SYENLTN RAVMDLNPV LSPN KLP IGI QV VFP LCK C P SKN Q LD KE I KY L	180					
Query 181 IT YVW KPGDNV SLS DK FGAS PEDIM SE NN YG QN FTA ANN LP V LIP V T RL PV L AR SP SD G	240					
Sbjct 181 IT YVW KPGDNV SLS DK FGAS PEDIM SE NN YG QN FTA ANN LP V LIP V T RL PV L AR SP SD G	240					
Query 241 RK GGIR LPV I I G I S L G C T L L V L V A L V L V Y V Y C L K M K T L N R S A S S A E T A D K L L S G V S G Y V	300					
Sbjct 241 RK GGIR LPV I I G I S L G C T L L V L V A L V L V Y V Y C L K M K T L N R S A S S A E T A D K L L S G V S G Y V	300					
Query 301 SK PT MY ET DAI ME AT MN IL SE Q CK I GE S V Y K AN IE GK V L AV K R FK ED VT EEL K I L Q KV NH G	360					
Sbjct 301 SK PT MY ET DAI ME AT MN IL SE Q CK I GE S V Y K AN IE GK V L AV K R FK ED VT EEL K I L Q KV NH G	360					
Query 361 NL VK LMG V S S D N G C N F V V Y E Y A E N G S L D E W L F S K C S D T S N S R A S L T W C Q R I S M A V D V A	420					
Sbjct 361 NL VK LMG V S S D N G C N F V V Y E Y A E N G S L D E W L F S K C S D T S N S R A S L T W C Q R I S M A V D V A	420					
Query 421 M GL Q YM H E H A Y P R I V H R D I T S S N I L L D S N F K A K I A N F S M A R T T N P M M P K I D V F A F G V V L	480					
Sbjct 421 M GL Q YM H E H A Y P R I V H R D I T S S N I L L D S N F K A K I A N F S M A R T T N P M M P K I D V F A F G V V L	480					
Query 481 I E L L T G R K A M T T K E N G E V V M L W K D I W K I F D Q E E N R E E R L K K W M D P K L E S Y Y P I D Y A L S L A	540					
Sbjct 481 I E L L T G R K A M T T K E N G E V V M L W K D I W K I F D Q E E N R E E R L K K W M D P K L E S Y Y P I D Y A L S L A	540					
Query 541 S L A V N C T A D K S L S R P T I A E I V L S L S L T Q P S P A T L E R S L T S S G L D V E A T Q I V T S I A A R	598					
Sbjct 541 S L A V N C T A D K S L S R P T I A E I V L S L S L T Q P S P A T L E R S L T S S G L D V E A T Q I V T S I A A R	598					

>gb|ADJ19106.1| Nod-factor receptor 5A [Glycine max]
Length=598

GENE ID: 100498858 NFR5a | Nod-factor receptor 5A [Glycine max]
(10 or fewer PubMed links)

Score = 1233 bits (3189), Expect = 0.0, Method: Compositional matrix adjust.
Identities = 597/598 (99%), Positives = 598/598 (100%), Gaps = 0/598 (0%)

Query 1 MAVFFPFLPLHSQILCLVIMLFSTNIVAQSQQDNRTNFSCPSDSSPPSCETYVTYIAQSPN	60					
Sbjct 1 MAVFFPFLPLHSQILCLVIMLFSTNIVAQSQQDNRTNFSCPSDSSPPSCETYVTYIAQSPN	60					

Sbjct	1	MAVFFPFLPLHSQIQLCLVIMLFSTNIVAQSQDNRNTFNSCPSDSPSCETYVTYIAQSPN	60
Query	61	FLSLTNISNIFDTSPLSIARASNLEPMDDKLVKDQVLVPVTCGCTGNRSFANISYEINQ	120
Sbjct	61	FLSLTNISNIFDTSPLSIARASNLEPMDDKLVKDQVLVPVTCGCTGNRSFANISYEINQ	120
Query	121	GDSFYFVATTSYENLTNWRAVMDLPVLSKPNKLPIGIQVVFPLFCPKCPSKNQLDEIKYL	180
Sbjct	121	GDSFYFVATTSYENLTNWRAVMDLPVLSKPNKLPIGIQVVFPLFCPKCPSKNQLDEIKYL	180
Query	181	ITYVWKPGDNVSLVSDKFGASPEDIMSENNYQGQFTAANNLPLVLPVTRLPVLARSPSDG	240
Sbjct	181	ITYVWKPGDNVSLVSDKFGASPEDIMSENNYQGQFTAANNLPLVLPVTRLPVLARSPSDG	240
Query	241	RKG GIRLP VII GIGS LGC TLL VLV LAV LL VVY CL MKT LNR SASSA ETAD KL LG SV GS YV	300
Sbjct	241	RKG GIRLP VII GIGS LGC TLL VLV LAV LL VVY CL MKT LNR SASSA ETAD KL LG SV GS YV	300
Query	301	SKPTMYETDAIMEATMNLSEQCKIGESVYKANIEGKVLA KRF KEDVTEELKILQKVNHG	360
Sbjct	301	SKPTMYETDAIMEATMNLSEQCKIGESVYKANIEGKVLA KRF KEDVTEELKILQKVNHG	360
Query	361	NLV KLMGVSS DNDGNC FVV YEAENG SLD EWLFSKSCSD TSNSRASL TW CQR ISMA DV A	420
Sbjct	361	NLV KLMGVSS DNDGNC FVV YEAENG SLD EWLFSKSCSD TSNSRASL TW CQR ISMA DV A	420
Query	421	MGL QYMHE HAYPRIH RDI TSSN ILLDSNF KAKI ANF SMART FTNPMP MKIDVFA FG VV L	480
Sbjct	421	MGL QYMHE HAYPRIH RDI TSSN ILLDSNF KAKI ANF SMART FTNPMP MKIDVFA FG VV L	480
Query	481	I ELLTGRKAMTT KENGEV VMLW KDI W KI FDQEENREER LKKWMDPKLES YYPIDYAL SLA	540
Sbjct	481	I ELLTGRKAMTT KENGEV VMLW KDI W KI FDQEENREER LKKWMDPKLES YYPIDYAL SLA	540
Query	541	SLAVNCTADKSLSRPTIAEIVLSSLSSLTQPSPATLERSLTSSGLDVEATQIVTSIAAR	598
Sbjct	541	SLAVNCTADKSLSRPTIAEIVLSSLSSLTQPSPATLERSLTSSGLDVEATQIVTSIAAR	598

>gb|ADJ19107.1| Nod-factor receptor 5A [Glycine max]
Length=598

GENE ID: 100498858 NFR5a | Nod-factor receptor 5A [Glycine max]
(10 or fewer PubMed links)

Score = 1231 bits (3184), Expect = 0.0, Method: Compositional matrix adjust.
Identities = 596/598 (99%), Positives = 598/598 (100%), Gaps = 0/598 (0%)

Query	1	MAVFFPFLPLHSQILCLVIMLFSTNIVAQSQDNRNTNSCPSPSDPPSCETYVTVIAQSPN	60
Sbjct	1	MAVFFPFLPLHSQILCLVIMLFSTNIVAQSQDNRNTNSCPSPSDPPSCETYVTVIAQSPN	60
Query	61	FLSLTNISNIFDTSPLSIARASNLEPMDDKLVKDQVLVLPVTGCGTGNRSFANISYEINQ	120
Sbjct	61	FLSLTNISNIFDTSPLSIARASNLEPMDDKLVKDQVLVLPVTGCGTGNRSFANISYEINQ	120
Query	121	GDSFYFVATTSYENLTNWRAVMDLPVLSPKNLPIGIVQVFPLFCPKCPSKNQLDEIKYL	180
Sbjct	121	GDSFYFVATTSYENLTNWRAVMDLPVLSPKNLPIGIVQVFPLFCPKCPSKNQLDEIKYL	180
Query	181	ITYWKPBDNVSLVSDKFGASPEDIMSENNYQGNFTAANNLPLVLIPTVTRLPVLARSPSDG	240
Sbjct	181	ITYWKPBDNVSLVSDKFGASPEDIMSENNYQGNFTAANNLPLVLIPTVTRLPVLARSPSDG	240
Query	241	RKGGLRPLVIIGISLGCTLLVLVLAFLVYVYCLMKTLNRSASSAETADKLLSGVGSYV	300
Sbjct	241	RKGGLRPLVIIGISLGCTLLVLVLAFLVYVYCLMKTLNRSASSAETADKLLSGVGSYV	300
Query	301	SKPTMYETDAIMEATMNLSEQCKIGESVYKANIEGKVLAVKRFKFEDVTEELKILQKVNHG	360
Sbjct	301	SKPTMYETDAIMEATMNLSEQCKIGESVYKANIEGKVLAVKRFKFEDVTEELKILQKVNHG	360
Query	361	NLVKLMGVSSNDGNCFVVYEAEAGNSLDEWLSFKSCSDTSNSRASLTWCQRISMADVVA	420
Sbjct	361	NLVKLMGVSSNDGNCFVVYEAEAGNSLDEWLSFKSCSDTSNSRASLTWCQRISMADVVA	420
Query	421	MGLQYMHEHAYPRIVHRDITSSNILLDSNSFKAKIANFSMARTFTNPMPMPKIDVFAFGVVL	480
Sbjct	421	MGLQYMHEHAYPRIVHRDITSSNILLDSNSFKAKIANFSMARTFTNPMPMPKIDVFAFGVVL	480
Query	481	IELLTGRKAMTTKENGEVVMLWKDIWIKIFDQEENREERLKKWMDPKLESYYPIDYALSLA	540
Sbjct	481	IELLTGRKA+TTKENGEVVMLWKDIWIKIFDQEENREERLKKWMDPKLESYYPIDYALSLA	540
Query	541	SLAVNCТАDKSLSRPTIAEIVLSLSLTLQPSPATLERSLTSSGLDVEATQIVTSIAAR	598
Sbjct	541	SLAVNCТАDKSLSRPTIAEIVLSLSLTLQPSPATLERSLTSSGLDVEATQIVTSIAAR	598

>gb|ADJ19112.1| Nod-factor receptor 5B [Glycine max]
Length=599

GENE ID: 100498857 NFR5b | Nod-factor receptor 5B [Glycine max]
(10 or fewer PubMed links)

Score	=	1106 bits (2861),	Expect	=	0.0,	Method:	Compositional matrix adjust.
Identities	=	563/599 (93%),	Positives	=	578/599 (96%),	Gaps	= 1/599 (0%)
Query	1	MAVFFPFLPLHSQILCLVLMLFSTNIVAQSQQQNDNRTNFSCPSDSSPPSC-ETYVTVTYIAQSP					59
Sbjct	1	MAVFF FPL SQILCLV-MLF TNIVAQSQQ N TNFSCPSDSSPP ETYVTVTYIAQSP					60
Query	60	NFLSLTNSINIFDTSPLSIARASNLEPMDDKLVLVKDQVLVLPVTCTGCTGNRSFANISYEIN					119
Sbjct	61	NFLSLT+ISNIFDTSPLSIARASNLEP DDKL+ DQVLV+PVTCGCTGNRSFANISYEIN					120
Query	120	QGDGSFYFVATTSYENLTNWRAVMDLNPVLSPNPKLPIGIVQVFPLFKCCKPSKNQLDKEIKY					179

Sbjct	121	GDSFYFVATTSYENLTNWR VMDLNP LSPN LPIG1QVVFPFLCKCP SKNQLDK IKY PGDSFYFVATTSYENLTNWRVMDLNPSLSPNTLP IGIQVVFPFLCKCP SKNQLDKGIKY	180
Query	180	LITYVWKPGDNVSLVSDKFGAS PEDIMSENNYQGNFTAANNLPVLIPVTRLPVLARSPSD LITYVW+P DNVSLVS+KFGAS PEDI+SENNYQGNFTAANNLPVLIPVTRLPVLARSPSD	239
Sbjct	181	LITYVWQPSDNVSLVSEKFGAS PEDILSENNYQGNFTAANNLPVLIPVTRLPVLARSPSD	240
Query	240	GRKGGIRLPVIIGISLGCTLLVLVLA VLLVYVYCLMKTLNR SASSAETADKL LSGVSGY RKG GIRLPVIIGISLGCTLLVLVLA VLLVYVYCLMKTLNR SASSAETADKL LSGVSGY	299
Sbjct	241	VRKGGIRLPVIIGISLGCTLLVVVLA VLLVYVYCLMKI SLSNR SASSAETADKL LSGVSGY	300
Query	300	VSKPTMYETDAIMEATMNL SEQCKIGESVYKANIEGKVLA VAKRKFEDVTEELKILQKVNH VSKPTMYETDAIMEATMNL SEQCKIGESVYKANIEGKVLA VAKRKFEDVTEELKILQKVNH	359
Sbjct	301	VSKPTMYETDAIMEATMNL SEQCKIGESVYKANIEGKVLA VAKRKFEDVTEELKILQKVNH	360
Query	360	GNLVKLMGVSSNDGNCFVVYEAE NGSLDEW LFSKCS DTSNSRASLTWCQR ISMA DV GN LVKLMGVSSNDGNCFVVYEAE NGSLDEW LFSKCS DTSNSRASLTWCQR ISMA DV	419
Sbjct	361	GNLVKLMGVSSNDGNCFVVYEAE NGSLDEW LFYKSCSDTS DRASLTWCQR ISIA DV	420
Query	420	AMGLQYMHEHAYPRIVHRDITSSNILLDSNFKAKIANFSMARTFTNPMPKIDVFAFGVV AMGLQYMHEHAYPRIVHRDI SSNILLDSNFKAKIANFSMARTFTNP MPKIDVFAFGVV	479
Sbjct	421	AMGLQYMHEHAYPRIVHRDIASSNILLDSNFKAKIANFSMARTFTNPMPKIDVFAFGVV	480
Query	480	LIELLTGRKAMTTKENGEVVMLW KDIW KIFDQEE NREERLK KWM DP KLESYY PIDY A LSL LIELLTGRKAMTTKENGEVVMLW KDIW KIFDQEE NREERLK KWM DP KLESYY PIDY A LSL	539
Sbjct	481	LIELLTGRKAMTTKENGEVVMLW KDIW KIFDQEE NREERLK KWM DP KLESYY PIDY A LSL	540
Query	540	ASLAVNCTADKSLSRPTIAEIVL SLSL TQP SPATLERSLTSSGLDVEATQIVTSIAAR ASLAVNCTADKSLSR TIAEIVL SLSL TQP SPATLERSLTSSGLDVEATQIVTSIAAR	598
Sbjct	541	ASLAVNCTADKSLSRSTIAEIVL SLSL TQP SPATLERSLTSSGLDVEATQIVTSIAAR	599

>gb|ADJ19111.1| Nod-factor receptor 5B [Glycine max]
Length=599

GENE ID: 100498857 NFR5B | Nod-factor receptor 5B [Glycine max]
(10 or fewer PubMed links)

Score = 1103 bits (2854), Expect = 0.0, Method: Compositional matrix adjust.	
Identities = 562/599 (93%), Positives = 577/599 (96%), Gaps = 1/599 (0%)	
Query 1 MAVFFPFLPLHSQILCLVIMLFSTNIVAQSQQDNRTNFSCPSDSSPPSC-ETYVYTYIAQSP 59 MAVFF FFLP HSQILCLVIMLFSTNIVAQSQQDNRTNFSCPSDSSPPSC-ETYVYTYIAQSP	
Sbjct 1 MAVFFSFLPLRSQILCLVIMLFSTNIVAQSQQTNETNFSCPSDSSPPSCETYVYTYIAQSP 60	
Query 60 NFLSLTNISNIFDTSPLSIARASNLEPMDDKLVQDVLLVPTCGCTGNRSFANISYEIN 119 NFLSLT+ISNIFDTSPLSIARASNLEP DDKL+ DQVLL+PVTCGCTGNRSFANISYEIN	
Sbjct 61 NFLSLTSNISNIFDTSPLSIARASNLEPEDDKLIAQDVLLIPVTCGCTGNRSFANISYEIN 120	
Query 120 QGDSFYFVATTSYENLTNWRAVMDLNPVLSPKNLP IGIQVVFPFLCKCP SKNQLDK IKY 179 GDSFYFVATTSYENLTNWRAVMDLNPVLSPKNLP IGIQVVFPFLCKCP SKNQLDK IKY	
Sbjct 121 PGDSFYFVATTSYENLTNWRVMDLNPSLSPNTLP IGIQVVFPFLCKCP SKNQLDKGIKY 180	
Query 180 LITYVWKPGDNVSLVSDKFGAS PEDIMSENNYQGNFTAANNLPVLIPVTRLPVLARSPSD LITYVW+P DNVSLVS+KFGAS PEDI+SENNYQGNFTAANNLPVLIPVTRLPVLARSPSD	239
Sbjct 181 LITYVWQPSDNVSLVSEKFGAS PEDILSENNYQGNFTAANNLPVLIPVTRLPVLARSPSD	240
Query 240 GRKGGIRLPVIIGISLGCTLLVLVLA VLLVYVYCLMKTLNR SASSAETADKL LSGVSGY RKG GIRLPVIIGISLGCTLLVLVLA VLLVYVYCLMKTLNR SASSAETADKL LSGVSGY	299
Sbjct 241 VRKGGIRLPVIIGISLGCTLLVVVLA VLLVYVYCLMKI SLSNR SASSAETADKL LSGVSGY	300
Query 300 VSKPTMYETDAIMEATMNL SEQCKIGESVYKANIEGKVLA VAKRKFEDVTEELKILQKVNH VSKPTMYETDAIMEATMNL SEQCKIGESVYKANIEGKVLA VAKRKFEDVTEELKILQKVNH	359
Sbjct 301 VSKPTMYETDAIMEATMNL SEQCKIGESVYKANIEGKVLA VAKRKFENVTEELKILQKVNH	360
Query 360 GNLVKLMGVSSNDGNCFVVYEAE NGSLDEW LFSKCS DTSNSRASLTWCQR ISMA DV GNLVKLMGVSSNDGNCFVVYEAE NGSLDEW LFSKCS DTSNSRASLTWCQR ISMA DV	419
Sbjct 361 GNLVKLMGVSSNDGNCFVVYEAE NGSLDEW LFYKSCSDTS DRASLTWCQR ISIA DV	420
Query 420 AMGLQYMHEHAYPRIVHRDITSSNILLDSNFKAKIANFSMARTFTNPMPKIDVFAFGVV AMGLQYMHEHAYPRIVHRDI SSNILLDSNFKAKIANFSMARTFTNP MPKIDVFAFGVV	479
Sbjct 421 AMGLQYMHEHAYPRIVHRDIASSNILLDSNFKAKIANFSMARTFTNPMPKIDVFAFGVV	480
Query 480 LIELLTGRKAMTTKENGEVVMLW KDIW KIFDQEE NREERLK KWM DP KLESYY PIDY A LSL LIELLTGRKAMTTKENGEVVMLW KDIW KIFDQEE NREERLK KWM DP KLESYY PIDY A LSL	539
Sbjct 481 LIELLTGRKAMTTKENGEVVMLW KDIW KIFDQEE NREERLK KWM DP KLESYY PIDY A LSL	540
Query 540 ASLAVNCTADKSLSRPTIAEIVL SLSL TQP SPATLERSLTSSGLDVEATQIVTSIAAR ASLAVNCTADKSLSR TIAEIVL SLSL TQP SPATLERSLTSSGLDVEATQIVTSIAAR	598
Sbjct 541 ASLAVNCTADKSLSRSTIAEIVL SLSL TQP SPATLERSLTSSGLDVEATQIVTSIAAR	599

>gb|ADJ19110.1| truncated Nod-factor receptor 5A [Glycine max]
Length=501

GENE ID: 100498858 NFR5A | Nod-factor receptor 5A [Glycine max]
(10 or fewer PubMed links)

Score = 1037 bits (2682), Expect = 0.0, Method: Compositional matrix adjust.	
Identities = 501/501 (100%), Positives = 501/501 (100%), Gaps = 0/501 (0%)	
Query 1 MAVFFPFLPLHSQILCLVIMLFSTNIVAQSQQDNRTNFSCPSDSSPPSCETYVYTYIAQSPN 60 MAVFFPFLPLHSQILCLVIMLFSTNIVAQSQQDNRTNFSCPSDSSPPSCETYVYTYIAQSPN	
Sbjct 1 MAVFFPFLPLHSQILCLVIMLFSTNIVAQSQQDNRTNFSCPSDSSPPSCETYVYTYIAQSPN 60	
Query 61 FLSLTNISNIFDTSPLSIARASNLEPMDDKLVQDVLLVPTCGCTGNRSFANISYEINQ 120 FLSLTNISNIFDTSPLSIARASNLEPMDDKLVQDVLLVPTCGCTGNRSFANISYEINQ	
Sbjct 61 FLSLTNISNIFDTSPLSIARASNLEPMDDKLVQDVLLVPTCGCTGNRSFANISYEINQ 120	
Query 121 GDSFYFVATTSYENLTNWRAVMDLNPVLSPKNLP IGIQVVFPFLCKCP SKNQLDK EIKYL GDSFYFVATTSYENLTNWRAVMDLNPVLSPKNLP IGIQVVFPFLCKCP SKNQLDK EIKYL	180
Sbjct 121 GDSFYFVATTSYENLTNWRAVMDLNPVLSPKNLP IGIQVVFPFLCKCP SKNQLDK EIKYL	180
Query 181 ITYVWKPGDNVSLVSDKFGAS PEDIMSENNYQGNFTAANNLPVLIPVTRLPVLARSPSDG ITYVWKPGDNVSLVSDKFGAS PEDIMSENNYQGNFTAANNLPVLIPVTRLPVLARSPSDG	240
Sbjct 181 ITYVWKPGDNVSLVSDKFGAS PEDIMSENNYQGNFTAANNLPVLIPVTRLPVLARSPSDG	240

Query	241	RKG GIRL PVI IGI S LG C T LL V L V A L V L V Y V Y C L K M K T L N R S A S S A E T A D K L L S G V S G Y V	300
Sbjct	241	RKG GIRL PVI IGI S LG C T LL V L V A L V L V Y V Y C L K M K T L N R S A S S A E T A D K L L S G V S G Y V	300
Query	301	SKP T M Y E T D A I M E A T M N L S E Q C K I G E S V Y K A N I E G K V L A V K R F K E D V T E E L K I L Q K V N H G	360
Sbjct	301	SKP T M Y E T D A I M E A T M N L S E Q C K I G E S V Y K A N I E G K V L A V K R F K E D V T E E L K I L Q K V N H G	360
Query	361	N L V K L M G V S S D N D G N C F V V Y E A N G S L D E W L F S K C S C D T S N S R A S L T W C Q R I S M A V D V A	420
Sbjct	361	N L V K L M G V S S D N D G N C F V V Y E A N G S L D E W L F S K C S C D T S N S R A S L T W C Q R I S M A V D V A	420
Query	421	M G L Q Y M H E H A Y P R I V H R D I T S S N I L L D S N F K A K I A N F S M A R T F T N P M M P K I D V F A F G V V L	480
Sbjct	421	M G L Q Y M H E H A Y P R I V H R D I T S S N I L L D S N F K A K I A N F S M A R T F T N P M M P K I D V F A F G V V L	480
Query	481	I E L L T G R K A M T T K E N G E V V M L	501
Sbjct	481	I E L L T G R K A M T T K E N G E V V M L	501

>gb|ABQ59613.1| NFR5b [Glycine max]
Length=515

Score = 957 bits (2475), Expect = 0.0, Method: Compositional matrix adjust.
Identities = 478/504 (94%), Positives = 491/504 (97%), Gaps = 0/504 (0%)

Query	95	Q V L L V P V T C G C T G N R S F A N I S Y E I N Q G D S F Y F V A T T S Y E N L T N W R A V M D L N P V L S P N K L P	154
Sbjct	12	Q V L L V P V T C G C T G N R S F A N I S Y E I N P G D S F N V F V A T T S Y E N L T N W R V V M D L N P S L S P N T L P	71
Query	155	I G I Q V V F P L F C K C P S K N Q L D K I K Y L I T Y V W + P D N V S L V S + K F G A S P E D I + S E N N Y Q N	214
Sbjct	72	I G I Q V V F P L F C K C P S K N Q L D K I K Y L I T Y V W Q P S D N V S L V S E K F G A S P E D I L S E N N Y Q N	131
Query	215	F T A A N N L P V L I P V T R L P V L A + P S D G R K G G I R L P V I I G I S L G C T L L V L V A L V L V Y V Y C L	274
Sbjct	132	F T A A N N L P V L I P V T R L P V L A Q F P S D V R K G G I R L P V I I G I S L G C T L L V V V L A L V L V Y V Y C L	191
Query	275	K M K T L N R S A S S A E T A D K L L S G V S G Y V S K P T M Y E T D A I M E A T M N L S E Q C K I G E S V Y K A N I E	334
Sbjct	192	K I K S L N R S A S S A E T A D K L L S G V S G Y V S K P T M Y E T D A I M E A T M N L S E K C K I G E S V Y K A N I E	251
Query	335	G K V L A V K R F K E D V T E E L K I L Q K V N H G N L V K L M G V S S D N D G N C F V V Y E A E N G S L D E W L F S	394
Sbjct	252	G K V L A V K R F K E N V T E E L K I L Q K V N H G N L V K L M G V S S D N D G N C F V V Y E A Q N G S L D E W L F S	311
Query	395	K C S C D T S N R S A S S A E T W C Q R I S M A V D V A M G L Q Y M H E H A Y P R I V H R D I T S S N I L L D S N F K A K I	454
Sbjct	312	K C S C D T S S R A S L T W C Q R I S A V D V A M G L Q Y M H E H A Y P R I V H R D I A S S N I L L D S N F K A K I	371
Query	455	A N F S M A R T F T N P M M P K I D V F A F G V V L I E L L T G R K A M T T K E N G E V V M L W K D I W K I F D Q E E N	514
Sbjct	372	A N F S M A R T F T N P T M P K I D V F A F G V V L I E L L T G R K A M T T K E N G E V V M L W K D I W K I F D Q E E N	431
Query	515	R E E R L K K W M D P K L E S Y Y P I D Y A L S A L S A V N C T A D K S L S R P T I A E I V L S L S L T T Q P S P A T	574
Sbjct	432	R E E R L K K W M D P K L E S Y Y P I D Y A L S A L S A V N C T A D K S L S R S T I A E I V L S L S L T T Q P S P A T	491
Query	575	L E R S L T S S G L D V E A T Q I V T S I A A R	598
Sbjct	492	L E R S L T S S G L D V E A T Q I V T S I A A R	515

>emb|CAE02593.1| SYM10 protein [Pisum sativum]
emb|CAE02594.1| SYM10 protein [Pisum sativum]
Length=594

Score = 899 bits (2322), Expect = 0.0, Method: Compositional matrix adjust.
Identities = 451/600 (75%), Positives = 505/600 (84%), Gaps = 8/600 (1%)

Query	1	M A V F F P L P L H S Q I L C L V I M L F S T N I V A Q S Q Q D N R T N F S C P S D S P P S C E T Y V T Y I A Q S P N	60
Sbjct	1	M A I F F - L P S S H A L F L A M F F V T N I S A Q P L Q I S G T N F S C P V D S P P S C E T Y V T Y F A R S P N	58
Query	61	F L S L T N I S I F D T S P L S I A R A S N L E P M D D K L V K D Q V L L V P V T C G C T G N R S F A N I S Y E I N Q	120
Sbjct	59	F L S L T N I S I F D T S P L S I A N S H + E D K L V + Q V L L + P V T C G C T N R F A N + Y I	118
Query	121	G D S F Y F V A T T S Y E N L T N W R A V M D L N P V L S P N K L P I G I Q V V F P L F C K C P S K N Q L D K E I K Y L	180
Sbjct	119	G D N Y F I V S T T S Y Q N L T N V Y E M E N P N P L S P N L L P E I K V V V L P C K C P S K N Q L S K G I K H L	178
Query	181	I T Y V W K P G D N V S L V S D K F G A S P E D I M S E N N Y Q N F T A A N N L P V L I P V T R L P V I A R S P S D G	240
Sbjct	179	I T Y V W Q A N D N V T R V S S K F G A S Q V D M F T E N N -- Q N F T A S T N V P I L P V T K L P V I D Q P S S N G	236
Query	241	R K G G I R L P V I I G I S L G C T L L V L V A L V L V Y V Y C L K M K T L N R S A S S A E T A D K L L S G V S G Y	299
Sbjct	237	R K N S T Q K P A F I I G I S L G C A F F V V V L T L S L V V Y V Y C L K M K R L N R S T L A E T A D K L L S G V S G Y	296
Query	300	V S K P T M Y E T D A I M E A T M N L S E Q C K I G E S V Y K A N I E G K V L A V K R F K E D V T E E L K I L Q K V N H	359
Sbjct	297	V S K P T M Y E M D A I M E A T M N L S E C K I G E S V Y K A N I G + V L A V K + K + D + E E L K I L Q K V N H	356
Query	360	G N L V K L M G V S S D N D G N C F V V Y E A E N G S L D E W L F S K C S C D T S N S R A S L T W C Q R I S M A V D V	419
Sbjct	357	G N L V K L M G V S S D N D G N C F + V Y E A E N G S L D E W L F S + S T S N S S L T W Q R I + + A V D V	415
Query	420	A M G L Q Y M H E H A Y P R I V H R D I T S S N I L L D S N F K A K I A N F S M A R T F T N P M M P K I D V F A F G V V	479
Sbjct	416	A + G L Q Y M H E H A Y P R I I H R D I T S S N I L L D S N F K A K I A N F S M A R T I T N M M P K I D V F A F G V V	475
Query	480	L I E L L T G R K A M T T K E N G E V V M L W K D I W K I F D Q E E N R E E R L K R W M D P K L E S Y Y P I D Y A L S L	539
Sbjct	476	L I E L L T G K K A I T T M E N G E V V I L W K D F W K I F D I E G N R E E S L R K W M D P K L E N F Y P I D N A L S L	535
Query	540	A S L A V N C T A D K S L S R P T I A E I V L S L S L T Q P S P A - T L E R S L T S S G L D V E A T Q I V T S I A A R	598

ASLAVNCTADKSLSRP+IAEIVL LSLL Q S LERSLT SGLDVEAT +VTSI AR
 Sbjct 536 ASLAVNCTADKSLSRPSIAEIVLCLSLLNQSSSEPMLERSLT-SGLDVEATHVVTISVAR 594

>emb|CAE02595.1| SYM10 protein [Pisum sativum]
 emb|CAE02596.1| SYM10 protein [Pisum sativum]
 gb|ADB45277.1| Nod factor recognition protein [Pisum sativum]
 Length=594

Score = 895 bits (2312), Expect = 0.0, Method: Compositional matrix adjust.
 Identities = 449/600 (74%), Positives = 504/600 (84%), Gaps = 8/600 (1%)

Query 1	MAVFFPFLPLHSQILCLVIMLFSTNIVAQSQQDNRTNFSCPSDSPSCETYVTVIAQSPN	60
Sbjct 1	MAVFF L S L L +M F TNI A Q + TNFSCP DSPPSCETYVTVY A+SPN	
Query 61	MAIFF--LPSSHLFLAMMFVFTNISAQPLQLSGTNFSCPVDSPPSCETYVTVYFARSPN	58
Sbjct 59	MAIFF--LPSSHLFLAMMFVFTNISAQPLQLSGTNFSCPVDSPPSCETYVTVYFARSPN	
Query 121	FLSLTNISNIFDSTSPLSIARASNLEPMDDKLVKDVQVLLVPVTCGCTGNRSFANISYEINQ	120
Sbjct 119	FLSLTNIS-I FD SPLSIA+ASN+E D KLV+ QVLL+PVTGCGT NR FAN +Y I	
Query 181	FLSLTNISDIFDMSPLSIAKASNIDEDKKLVEGQVLLIPVTCGCTRNRYFANFTTYIKL	118
Sbjct 179	FLSLTNISDIFDMSPLSIAKASNIDEDKKLVEGQVLLIPVTCGCTRNRYFANFTTYIKL	
Query 241	GDSFYFVATTSYENLTNWRRAVMMDLNPVLSPNPKLPIGIQVVFPLFCPKPSKNQLDEIKYL	180
Sbjct 237	GDSFYFVATTSYENLTNWRRAVMMDLNPVLSPNPKLPIGIQVVFPLFCPKPSKNQLK 1K+L	
Query 300	GDNYFIVSTTSQYQNLTNYVEMENFNPNLSPNLLPPEIKVVVPLFCKCPSKNQLSKGIKHL	178
Sbjct 297	GDNYFIVSTTSQYQNLTNYVEMENFNPNLSPNLLPPEIKVVVPLFCKCPSKNQLSKGIKHL	
Query 360	ITYVWKGPDNVSLVSDKFAGSPEDIMSENNYGNFTAANNLPVLIPVTRLPVLARSPODG	240
Sbjct 357	ITYVWKGPDNVSLVSDKFAGSPEDIMSENNYGNFTAANNLPVLIPVTRLPVLARSPODG	
Query 420	ITVWKGPDNVSLVSDKFAGSPEDIMSENNYGNFTAANNLPVLIPVTRLPVLARSPODG	236
Sbjct 357	ITVWKGPDNVSLVSDKFAGSPEDIMSENNYGNFTAANNLPVLIPVTRLPVLARSPODG	
Query 480	RKGIGRLPV-IIGISLGCTLLVLVLAFLVYVYCLMKTLNRSSAETADKLLSGVGSGY	299
Sbjct 466	RKGIGRLPV-IIGISLGCTLLVLVLAFLVYVYCLMKTLNRSSAETADKLLSGVGSGY	
Query 540	RKGIGRLPV-IIGISLGCTLLVLVLAFLVYVYCLMKTLNRSSAETADKLLSGVGSGY	296
Sbjct 536	RKGIGRLPV-IIGISLGCTLLVLVLAFLVYVYCLMKTLNRSSAETADKLLSGVGSGY	
Query 598	RKNSTQKPAFIIGISLGCAFFVVVLTLSLVYVYCLMKRNLNRSTAETADKLLSGVGSGY	299
Sbjct 594	RKNSTQKPAFIIGISLGCAFFVVVLTLSLVYVYCLMKRNLNRSTAETADKLLSGVGSGY	
Query 598	ASLAVNCTADKSLSRPTIAEIVL SLLTQPSP-A T L E R S L T S S G L D V E A T Q I V T S I A A R	598
Sbjct 536	ASLAVNCTADKSLSRPTIAEIVL SLLTQPSP-A T L E R S L T S S G L D V E A T Q I V T S I A A R	
Query 598	ASLAVNCTADKSLSRPSIAEIVLCLSLLNQSSSEPMLERSLT-SGLDVEATHVVTISVAR	594
Sbjct 594	ASLAVNCTADKSLSRPSIAEIVLCLSLLNQSSSEPMLERSLT-SGLDVEATHVVTISVAR	

>emb|CAE02597.1| Nod-factor receptor 5 [Lotus japonicus]
 emb|CAE02598.1| Nod-factor receptor 5 [Lotus japonicus]
 Length=595

GENE ID: 100034751 NFR5 | Nod-factor receptor 5 [Lotus japonicus]
 (10 or fewer PubMed links)

Score = 875 bits (2262), Expect = 0.0, Method: Compositional matrix adjust.
 Identities = 449/601 (74%), Positives = 500/601 (83%), Gaps = 9/601 (1%)

Query 1	MAVFFPFLPLHSQILCLVIMLFSTNIVAQSQQDNRTNFSCPSDSPSCETYVTVIAQSPN	60
Sbjct 1	MAVFF L S L L +M F TNI A Q + TNFSCP DSPPSCETYVTVY A+SPN	
Query 61	MAVFF--LPSSHLFLAMMFVFTNISAQPLQLSGTNFSCPVDSPPSCETYVTVYFARSPN	58
Sbjct 59	MAVFF--LPSSHLFLAMMFVFTNISAQPLQLSGTNFSCPVDSPPSCETYVTVYFARSPN	
Query 121	FLSLTNISNIFDSTSPLSIARASNLEPMDDKLVKDVQVLLVPVTCGCTGNRSFANISYEINQ	120
Sbjct 119	FLSLTNIS-I FD SPLSIA+ASN+E D KLV+ QVLL+PVTGCGT NR FAN +Y I	
Query 181	FLSLTNISDIFDMSPLSIAKASNIDEDKKLVEGQVLLIPVTCGCTRNRYFANFTTYIKL	118
Sbjct 179	FLSLTNISDIFDMSPLSIAKASNIDEDKKLVEGQVLLIPVTCGCTRNRYFANFTTYIKL	
Query 241	GDSFYFVATTSYENLTNWRRAVMMDLNPVLSPNPKLPIGIQVVFPLFCPKPSKNQLDEIKYL	180
Sbjct 237	GDSFYFVATTSYENLTNWRRAVMMDLNPVLSPNPKLPIGIQVVFPLFCPKPSKNQLK 1K+L	
Query 300	GDNYFIVSTTSQYQNLTNYVEMENFNPNLSPNLLPPEIKVVVPLFCKCP SKNQLSKGIKHL	178
Sbjct 297	GDNYFIVSTTSQYQNLTNYVEMENFNPNLSPNLLPPEIKVVVPLFCKCP SKNQLSKGIKHL	
Query 360	ITYVWKGPDNVSLVSDKFAGSPEDIMSENNYGNFTAANNLPVLIPVTRLPVLARSPODG	240
Sbjct 357	ITYVWKGPDNVSLVSDKFAGSPEDIMSENNYGNFTAANNLPVLIPVTRLPVLARSPODG	
Query 420	ITVWKGPDNVSLVSDKFAGSPEDIMSENNYGNFTAANNLPVLIPVTRLPVLARSPODG	236
Sbjct 357	ITVWKGPDNVSLVSDKFAGSPEDIMSENNYGNFTAANNLPVLIPVTRLPVLARSPODG	
Query 480	RKGIGRLPV-IIGISLGCTLLVLVLAFLVYVYCLMKTLNRSSAETADKLLSGVGSGY	299
Sbjct 466	RKGIGRLPV-IIGISLGCTLLVLVLAFLVYVYCLMKTLNRSSAETADKLLSGVGSGY	
Query 540	RKGIGRLPV-IIGISLGCTLLVLVLAFLVYVYCLMKTLNRSSAETADKLLSGVGSGY	296
Sbjct 536	RKGIGRLPV-IIGISLGCTLLVLVLAFLVYVYCLMKTLNRSSAETADKLLSGVGSGY	
Query 598	RKNSTQKPAFIIGISLGCAFFVVVLTLSLVYVYCLMKRNLNRSTAETADKLLSGVGSGY	299
Sbjct 594	RKNSTQKPAFIIGISLGCAFFVVVLTLSLVYVYCLMKRNLNRSTAETADKLLSGVGSGY	
Query 598	ASLAVNCTADKSLSRPTIAEIVL SLLTQPSP-A T L E R S L T S S G L D V E A T Q I V T S I A A R	598
Sbjct 536	ASLAVNCTADKSLSRPTIAEIVL SLLTQPSP-A T L E R S L T S S G L D V E A T Q I V T S I A A R	
Query 598	ASLAVNCTADKSLSRPSIAEIVLCLSLLNQSSSEPMLERSLT-SGLDVEATHVVTISVAR	594
Sbjct 594	ASLAVNCTADKSLSRPSIAEIVLCLSLLNQSSSEPMLERSLT-SGLDVEATHVVTISVAR	

>**gb|ABF50224.1| Nod factor perception protein [Medicago truncatula]**
Length=595

Score = 864 bits (2232), Expect = 0.0, Method: Compositional matrix adjust.
Identities = 429/577 (74%), Positives = 485/577 (84%), Gaps = 6/577 (1%)

Query 24	TNIVAQSQQDNRTNFSCPSDPPSCTYVTYIAQSPNFLSLTNISNIFDTSPLSIARASN	83
Sbjct 23	TNI AQ + TNF+CP DSPSCTETV Y AQPSPNFLSL+NIS+IF+ SPL IA+ASN	
Query 84	TNISAQPLYISETNFTCPVDSPSCTETVAYRAQSPNFLSLNSIDIFNLSPLRIAKASN	82
Sbjct 83	+E D KL+ DQ+LLPVTCGCT N SFANI+Y I QGD+F+ ++ TSY+NLTN+ IEAEDKKLIPDQLLLPVTCGCTKHNHSFANITYSIKQGDNNFFILSITSYQNLNTYLEFKN	142
Query 144	LEPMDDKLVLKDQVLLPVTCGCTGNRSFANISEYEINQGDSFYFVATTSYENLTNWRAVMD	143
Sbjct 143	+E D KL+ DQ+LLPVTCGCT N SFANI+Y I QGD+F+ ++ TSY+NLTN+ NP LSP LP+ +V PLFCCKPSKNQL+K IKYLITYVW+ DNV+LVS KFGAS	203
Query 204	FNPNLSPTLLPLDTKVSVPLFCCKPSKNQLNKGIKYLITYVWQDNDNVTLVSSKFGASQV	202
Sbjct 203	DIMSENNYQGNFTAANNLPLVLIPTVRLPVLARSPLSDGRKGIR-LPVIIGISLGCTLLVL	262
Query 263	EMLAENNH--NFTASTNRNSVLIPTVSLPKLDQPSNSNGRKSSSQNLALIIGISLGSAFFIL	260
Sbjct 261	VLA LLVYVYCLMKMKTLNRSASSAETADKLLSGVGSGYVSKPTMYETDAIMEATMNLSEQC	322
Query 323	VLTLSSLVYVYCLMKMKTLNRSASSAETADKLLSGVGSGYVSKPTMYETDAIMEATMNLSEQC	320
Sbjct 321	KIGESVYKANIEGKVLAVKRFKEDVTEELKILQKVNHGNLVKLMGVSSDNDGNCVYYEY	382
Query 383	KIGESVYKANI+G+VLA+K+D +EELKILQKVNHGNLVKLMGVSSDNDGNCF+VVEY	380
Sbjct 381	KIGESVYKANIDGRVLAVKVKIKKDAEELKILQKVNHGNLVKLMGVSSDNDGNCFLVYEEY	442
Query 443	AENGSLDEEWLFSE+S TSNS SLTW QRI+A+DVA+GLQYMHEH YPRI+HRDIT+S	439
Sbjct 440	AENGSL+EWLFS+E SKTSNSVSLWSQRITIAMDVAGLQYMHEHTYPRIIHRDITTS	502
Query 503	NILLDSNFKAKIANFSMARTFTNPNMPKIDVFAFGVVLIELLTGRKAMTTKENGEVVILW	499
Sbjct 500	NILLDSNFKAKIANFSMARTFTNPNMPKIDVFAFGVVLIELLTGRKAMTTKENGEVVILW	562
Query 563	KD1WKIFDQEENREERLKKWMDPKLES+YPID ALSLASLAVNCTADKSLSRPTIAEIVL	559
Sbjct 560	KDFWKIFDLEGNREREERLKKWMDPKLES+YPID ALNSLASLAVNCTADKSLSRPTIAEIVL	598

>**emb|CAO02956.1| LysM-domain containing receptor-like kinase [Medicago truncatula]**
var. truncatula
Length=498

Score = 761 bits (1966), Expect = 0.0, Method: Compositional matrix adjust.
Identities = 370/497 (74%), Positives = 423/497 (85%), Gaps = 4/497 (0%)

Query 46	PSCTETYVYIAQSPNFLSLTNISNIFDTSPLSIARASNLEPMDDKLVQDQVLLPVTCGC	105
Sbjct 4	PSCTETYV Y AQPSPNFLSL+NIS+IF+ SPL IA+ASN+E D KL+ DQ+LLPVTCGC	63
Query 106	TGNRSFANISEYEINQGDSFYFVATTSYENLTNWRAVMDLNPVLSPNPKLPIGIQVVPLFC	165
Sbjct 64	T N SFANI+Y I QGD+F+ ++ TSY+NLTN+ + NP LSP LP+ +V PLFC	123
Query 166	TKHNSFANITYSIKQGDNNFILSITSYQNLNTYLEFKNFPNLSPLTLLPLDTKVSVPLFC	225
Sbjct 124	KCPSKNQLDKEIKYLITYVWQDNDNVTLVSSKFGASQVEMLAENNH--NFTASTNRSLI	181
Query 226	KCPSKNQL+K IKYLITYVW+ DNV+LVS KFGAS +++ENN+ NFTA+ N VLI	284
Sbjct 182	PVTLPLVLRSPSLSGRKGIR-LPVIIGISLGCTLLVVLVLA VLLVYVYCLMKTLNRSAS	241
Query 285	PVTLPLVLRSPSLSGRKGIR-LPVIIGISLGCTLLVVLVLA VLLVYVYCLMKTLNRSAS	344
Sbjct 242	+EELKILQKVNHGNLVKLMGVSSDNDGNCF+VVEY AENGSL+EWLFS+S TSNS	301
Query 345	SAETADKLLSGVGSGYVSKPTMYETDAIMEATMNLSEQCKIGESVYKANIEGKVLAVKRFK	404
Sbjct 302	+EELKILQKVNHGNLVKLMGVSSDNDGNCF+VVEY AENGSL+EWLFS+S TSNS	360
Query 405	EDVTEELKILQKVNHGNLVKLMGVSSDNDGNCFVYYEYAENGSLDEWLFSKCSDTDNSR	464
Sbjct 361	+EELKILQKVNHGNLVKLMGVSSDNDGNCF+VVEY AENGSL+EWLFS+S TSNS	420
Query 465	EDVTEELKILQKVNHGNLVKLMGVSSDNDGNCFVYYEYAENGSLDEWLFSKCSDTDNSR	524
Sbjct 421	+EELKILQKVNHGNLVKLMGVSSDNDGNCF+VVEY AENGSL+EWLFS+S TSNS	480
Query 525	NPMPKIDVFAFGVVLIELLTGRKAMTTKENGEVVILWWDK1WKIFDQEENREERLKKWMD	541
Sbjct 481	+EELKILQKVNHGNLVKLMGVSSDNDGNCF+VVEY AENGSL+EWLFS+S TSNS	497

>**emb|CAO02958.1| LysM-domain containing receptor-like kinase [Medicago truncatula]**
var. truncatula
Length=492

Score = 754 bits (1948), Expect = 0.0, Method: Compositional matrix adjust.
Identities = 367/494 (74%), Positives = 420/494 (85%), Gaps = 4/494 (0%)

Query 49	ETTYVYIAQSPNFLSLTNISNIFDTSPLSIARASNLEPMDDKLVQDQVLLPVTCGCTGN	108
Sbjct 1	ETTYVYIAQSPNFLSL+NIS+IF+ SPL IA+ASN+E D KL+ DQ+LLPVTCGCTGN	60
Query 109	TETTYVYIAQSPNFLSLTNISNIFDTSPLSIARASNLEPMDDKLVQDQVLLPVTCGCTGN	168
Sbjct 61	ETTYVYIAQSPNFLSL+NIS+IF+ SPL IA+ASN+E D KL+ DQ+LLPVTCGCTGN	120
Query 169	RSFANISEYEINQGDSFYFVATTSYENLTNWRAVMDLNPVLSPNPKLPIGIQVVPLFC	228
Sbjct 169	HSFANITYSIKQGDNNFFILSITSYQNLNTYLEFKNFPNLSPLTLLPLDTKVSVPLFC	228

Sbjct 121 SKNQL+K IKYLITYVW+ DNV+LVS KFGAS +++ENN+ NFTA+ N VLIPVT
 Sbjct 121 SKNQLNKG IKYLITYVWQDNDNVTLVSSKFGASQVEMLAENN--NFTASTNRSLIPVT 178

Query 229 RLPVLARSPSDGRKGGIR-LPVIIGISLGCTLLVVLAVLLVYVYCLMKTLNRSASSAE
 LP L + S+GRK + L +IIGISLG +LVL + LVVYCLMK LNRS SS+E 287

Sbjct 179 SLPKLDQPSNSGRKSSQNLALIIGISLSAFFILVLTSLVYVYCLMKRNLNSTSSSE 238

Query 288 TADKLLSGVSGYVSKPTMYETDAIMEATMNLSEQCKIGESVYKANIEGKVLAVKRFKEDV
 TADKLLSGVSGYVSKPTMYE DAIME TMNL+ CKIGESVYKANI+G+VLAVK+ K+D 347

Sbjct 239 TADKLLSGVSGYVSKPTMYEIDAIMEGTMNLSDNCKIGESVYKANIDGRVLAVKKIKKDA 298

Query 348 TEELKILQKVNHNGLVKLMGVSSNDGNCFVYEAENGSLDEWLFSKCSDTNSRASL
 +TEELKILQKVNHNGLVKLMGVSSNDGNCF+VYEYAENGSL+BWLFS+S TSNS SL 407

Sbjct 299 SEELKILQKVNHNGLVKLMGVSSNDGNCFLVYEEAENGSLEEWLFSSES-SKTSNSVVSL 357

Query 408 TWCRISMAVDVAMGLQYMHEHYPRIHVDITSSNILLDSNEAKIANFSMARTFTNPM 467

TW QRI+A+DVA+GLQYMHEH YPRI+HRDIT+SNILL SNFKAKIANF MART TN M

Sbjct 358 TWSQRITIAMDVAILGLQYMHEHTYPRIHVDITTSNILLGSNFKAKIANFGMARTSTNSM 417

Query 468 MPKIDVFAGVVILIETGRKAMTTKENGEVVMLWKDIWKIFDQEENREERLKWKMDPKL 527

MPKIDVFAGVVILIETLTGKAMTTKENGEVV+LWKD WKIFD E NREERL+KWMMDPKL

Sbjct 418 MPKIDVFAGVVILIETLTGKAMTTKENGEVVLWKDFWKIFDLEGNRERLWKWMMDPKL 477

Query 528 ESYYPIDYALS LAS 541

ES+YPID ALS+AS

Sbjct 478 ESFYPIDNALSMAS 491

>**emb|CAO02933.1|** LysM-domain containing receptor-like kinase [Medicago truncatula
 var. truncatula]
emb|CAO02934.1| LysM-domain containing receptor-like kinase [Medicago truncatula
 var. truncatula]
emb|CAO02935.1| LysM-domain containing receptor-like kinase [Medicago truncatula
 var. truncatula]

10 more sequence titles

emb|CAO02938.1| LysM-domain containing receptor-like kinase [Medicago truncatula
 var. truncatula]
emb|CAO02939.1| LysM-domain containing receptor-like kinase [Medicago truncatula
 var. truncatula]
emb|CAO02952.1| LysM-domain containing receptor-like kinase [Medicago truncatula
 var. longicauleata]
emb|CAO02955.1| LysM-domain containing receptor-like kinase [Medicago truncatula
 var. truncatula]
emb|CAO02957.1| LysM-domain containing receptor-like kinase [Medicago truncatula
 var. truncatula]
emb|CAO02959.1| LysM-domain containing receptor-like kinase [Medicago truncatula
 var. truncatula]
emb|CAO02967.1| LysM-domain containing receptor-like kinase [Medicago truncatula
 var. truncatula]
emb|CAO02971.1| LysM-domain containing receptor-like kinase [Medicago truncatula
 var. truncatula]
emb|CAO02972.1| LysM-domain containing receptor-like kinase [Medicago truncatula
 var. truncatula]
emb|CAO02973.1| LysM-domain containing receptor-like kinase [Medicago truncatula
 var. truncatula]

Length=487

Score = 747 bits (1928), Expect = 0.0, Method: Compositional matrix adjust.
 Identities = 363/489 (74%), Positives = 416/489 (85%), Gaps = 4/489 (0%)

Query 54 YIAQSPNFLSLTNISNIFDTSPSIARASNLEPMDDKLVKDQVLLPVTCGCTGNRSFAN 113
 Y AQSPNFLSL+NIS+IF+ SPL IA+ASN+E D KL+ DQ+LLPVTCGCT N SFAN
 Sbjct 1 YRAQSPNFLSLNSIDFNLSPLRIAKASNIEADKKLIPDQLLVPVTCGCTKNHSFAN 60

Query 114 ISYEINQGDSFYFVATTYSYENLNWRAVMIDLNPVLSNPKLPIG1QVVFPLFCKCPSKNQL 173
 I+Y I QGD+F+ ++ TSY+NLTN+ + NP LSP LP+ +V PLFCKCPSKNQL
 Sbjct 61 ITYSIKQGDNNFFILSITSYQNLTNYLEFKNFPNLSPTLLPLDKVSVPLFCKCPSKNQL 120

Query 174 DKEIKYLITYVWKPGDNVSLVSDKFGASPEDIMSENNYGQNFTAANNLPVLPVTRLPVL 233
 +K IKYLITYVW+ DNV+LVS KFGAS +++ENN+ NFTA+ N VLIPVT LP L
 Sbjct 121 NKGIKYLITYVWQDNDNVTLVSSKFGASQVEMLAENN--NFTASTNRSLIPVTSPLPKL 178

Query 234 ARSPSDGRKGGIR-LPVIIGISLGCTLLVVLAVLLVYVYCLMKTLNRSASSAETADKL 292
 + S+GRK + L +IIGISLG +LVL + LVVYCLMK LNRS SS+ETADKL
 Sbjct 179 DQPSSNSGRKSSQNLALIIGISLSAFFILVLTSLVYVYCLMKRNLNSTSSSETADKL 238

Query 293 LSGVSGYVSKPTMYETDAIMEATMNLSEQCKIGESVYKANIEGKVLAVKRFKEDVTEELK 352
 LSGVSGYVSKPTMYE DAIME TMNL+ CKIGESVYKANI+G+VLAVK+ K+D +EELK
 Sbjct 239 LSGVSGYVSKPTMYEIDAIMEGTMNLSDNCKIGESVYKANIDGRVLAVKKIKKDAEELK 298

Query 353 ILQKVNHNGLVKLMGVSSNDGNCFVYEAENGSLDEWLFSKCSDTNSRASLTWCQR 412
 ILQKVNHNGLVKLMGVSSNDGNCF+VYEYAENGSL+BWLFS+S TSNS SLTW QR
 Sbjct 299 ILQKVNHNGLVKLMGVSSNDGNCFLVYEEAENGSLEEWLFSSES-SKTSNSVVSLLTWSQR 357

Query 413 ISMAVDVAMGLQYMHEHYPRIHVDITSSNILLDSNFKAKIANFSMARTFTNPMMPKID 472
 I+A+DVA+GLQYMHEH YPRI+HRDIT+SNILL SNFKAKIANF MART TN MMMPKID
 Sbjct 358 ITIAMDVAILGLQYMHEHTYPRIHVDITTSNILLGSNFKAKIANFGMARTSTNSMMPKID 417

Query 473 VFAGVVILIETLTGKAMTTKENGEVVMLWKDIWKIFDQEENREERLKWKMDPKLESYYP 532
 VFAGVVILIETLTGKAMTTKENGEVV+LWKD WKIFD E NREERL+KWMMDPKLES+YYP
 Sbjct 418 VFAGVVILIETLTGKAMTTKENGEVVLWKDFWKIFDLEGNRERLWKWMMDPKLESYYP 477

Query 533 IDYALSLAS 541
 ID ALS+AS
 Sbjct 478 IDNALSMAS 486

>**emb|CAO02951.1|** LysM-domain containing receptor-like kinase [Medicago truncatula
 var. truncatula]
 Length=487

Score = 745 bits (1924), Expect = 0.0, Method: Compositional matrix adjust.
 Identities = 363/489 (74%), Positives = 415/489 (84%), Gaps = 4/489 (0%)

Query 54 YIAQSPNFLSLTNISNIFDTSPSIARASNLEPMDDKLVKDQVLLPVTCGCTGNRSFAN 113
 Y AQSPNFLSL+NIS+IF+ SPL IA+ASN+E D KL+ DQ+LLPVTCGCT N SFAN
 Sbjct 1 YRAQSPNFLSLNSIDFNLSPLRIAKASNIEADKKLIPDQLLVPVTCGCTKNHSFAN 60

Query 114 ISYEINQGDSFYFVATTYSYENLTNWRAVMMDLNPLSPNKLPIGIQVVFPFLCKCPSKNQL 173
 Sbjct 61 ITYSIKQGDNNFFILSITSYQNLNTYLEFKFNPNLSPTLLPLDTKVSVPFLCKCPSKNQL 120

Query 174 DKEIKYLITYVWKPGDNVSLVSDKFGASPEDIMSENNYQGNFTAANNLPVLIPVTRLPVL 233
 Sbjct 121 NKGIKYLITYVWQNDNDNVTLVSSKFGASQVEMIENNHH--NFTASTNRSVLIPVTSPLKL 178

Query 234 ARSPSDGRKGIR-LPVIIGISLGCTLLVLAVALVYVYCLMKTLNRSASSAETADKL 292
 Sbjct 179 +S+GRK + L +IIGISLG +LVL + LVVYVCLMKM LNRS SS+ETADKL 238

Query 293 LSGVSGYVSKPTMYETDAIMEATMNLSEQCKIGESVYKANIEGKVLAVKRFKEDVTEELK 352
 Sbjct 239 LSGVSGYVSKPTMYEIDAIMEGTNTLSDNCKIGESVYKANIDGRVLAVKKIKKDAEELK 298

Query 353 ILQKVNHGNLVKLGMVSSDNGNCFCVYVYEAENGSLDEWLFSKSCSDTSNSRASLTWCQR 412
 Sbjct 299 ILQKVNHGNLVKLGMVSSDNGNCFCVYVYEAENGSL+EWLFS+S TSNS SLTW QR 357

Query 413 ISMAVDVAMGLQYMHEHAYPRIHRDITSSNILLDSNFKAKIANFSMARTFTNPMMPKID 472
 Sbjct 358 I+I+A+DVA+GLQYMHEH YPRI+HRDIT+SNILL SNFKAKIANF MART TN MMPKID 417

Query 473 VFAFGVVLIELLTGRKAMTTKENGEVVMWLWDIWKIFDQEENREERLKKWMDPKLESYYP 532
 Sbjct 418 VFAFGVVLIELLTGKAMTTKENGEVVLWKFWKIFDLEGNRERLRKWMDPKLESYYP 477

Query 533 IDYALSLAS 541
 Sbjct 478 IDNALSLAS 486

>**emb|CAO02940.1|** LysM-domain containing receptor-like kinase [Medicago truncatula]
 var. truncatula]
 Length=487

Score = 745 bits (1923), Expect = 0.0, Method: Compositional matrix adjust.
 Identities = 363/489 (74%), Positives = 415/489 (84%), Gaps = 4/489 (0%)

Query 54 YIAQSPNFLSLTNISNIFDTSPLSIARASNLEPMDDKLVLKDQVLLPVTCGCTGNRSFAN 113
 Sbjct 1 YRAQSPNFLSLNISDIFNLSPLRIAKASNIEADKKLIPDQLLLVPVTCGCTKNHSFAN 60

Query 114 ISYEINQGDSFYFVATTYSYENLTNWRAVMMDLNPLSPNKLPIGIQVVFPFLCKCPSKNQL 173
 Sbjct 61 ITYSIKQGDNNFFILSITSYQNLNTYLEFKFNPNLSPTLLPLDTKVSVPFLCKCPSKNQL 120

Query 174 DKEIKYLITYVWKPGDNVSLVSDKFGASPEDIMSENNYQGNFTAANNLPVLIPVTRLPVL 233
 Sbjct 121 NKGIKYLITYVWQNDNDNVTLVSSKFGASQVEMIENNHH--NFTASTNRSVLIPVTSPLKL 178

Query 234 ARSPSDGRKGIR-LPVIIGISLGCTLLVLAVALVYVYCLMKTLNRSASSAETADKL 292
 Sbjct 179 +S+GRK + L +IIGISLG +LVL + LVVYVCLMKM LNRS SS+ETADKL 238

Query 293 LSGVSGYVSKPTMYETDAIMEATMNLSEQCKIGESVYKANIEGKVLAVKRFKEDVTEELK 352
 Sbjct 239 LSGVSGYVSKPTMYEIDAIMEGTNTLSDNCKIGESVYKANIDGRVLAVKKIKKDAEELK 298

Query 353 ILQKVNHGNLVKLGMVSSDNGNCFCVYVYEAENGSLDEWLFSKSCSDTSNSRASLTWCQR 412
 Sbjct 299 ILQKVNHGNLVKLGMVSSDNGNCFCVYVYEAENGSL+EWLFS+S TSNS SLTW QR 357

Query 413 ISMAVDVAMGLQYMHEHAYPRIHRDITSSNILLDSNFKAKIANFSMARTFTNPMMPKID 472
 Sbjct 358 I+I+A+DVA+GLQYMHEH YPRI+HRDIT+SNILL SNFKAKIANF MART TN MMPKID 417

Query 473 VFAFGVVLIELLTGRKAMTTKENGEVVMWLWDIWKIFDQEENREERLKKWMDPKLESYYP 532
 Sbjct 418 VFAFGVVLIELLTGKAMTTKENGEVVLWKFWKIFDLEGNRERLRKWMDPKLESYYP 477

Query 533 IDYALSLAS 541
 Sbjct 478 IDNALSLAS 486

>**emb|CAO02941.1|** LysM-domain containing receptor-like kinase [Medicago truncatula]
 var. truncatula]
emb|CAO02970.1| LysM-domain containing receptor-like kinase [Medicago truncatula]
 var. truncatula]
 Length=487

Score = 744 bits (1922), Expect = 0.0, Method: Compositional matrix adjust.
 Identities = 362/489 (74%), Positives = 415/489 (84%), Gaps = 4/489 (0%)

Query 54 YIAQSPNFLSLTNISNIFDTSPLSIARASNLEPMDDKLVLKDQVLLPVTCGCTGNRSFAN 113
 Sbjct 1 YRAQSPNFLSLNISDIFNLSPLRIAKASNIEADKKLIPDQLLLVPVTCGCTKNHSFAN 60

Query 114 ISYEINQGDSFYFVATTYSYENLTNWRAVMMDLNPLSPNKLPIGIQVVFPFLCKCPSKNQL 173
 Sbjct 61 ITYSIKQGDNNFFILSITSYQNLNTYLEFKFNPNLSPTLLPLDTKVSVPFLCKCPSKNQL 120

Query 174 DKEIKYLITYVWKPGDNVSLVSDKFGASPEDIMSENNYQGNFTAANNLPVLIPVTRLPVL 233
 Sbjct 121 NKGIKYLITYVWQNDNDNVTLVSSKFGASQVEMIENNHH--NFTASTNRSVLIPVTSPLKL 178

Query 234 ARSPSDGRKGIR-LPVIIGISLGCTLLVLAVALVYVYCLMKTLNRSASSAETADKL 292
 Sbjct 179 +S+GRK + L +IIGISLG +LVL + LVVYVCLMKM LNRS SS+ETADKL 238

Query 293 LSGVSGYVSKPTMYETDAIMEATMNLSEQCKIGESVYKANIEGKVLAVKRFKEDVTEELK 352
 Sbjct 239 LSGVSGYVSKPTMYEIDAIMEGTNTLSDNCKIGESVYKANIDGRVLAVKKIKKDAEELK 298

Query 353 ILQKVNHGNLVKLGMVSSDNGNCFCVYVYEAENGSLDEWLFSKSCSDTSNSRASLTWCQR 412

Sbjct	299	ILQKVNHNGLVKLMLGVSSDNDGNCF+VYEYAENGSL+EWLFS+S S TSNS SLTW QR ILQKVNHNGLVKLMLGVSSDNDGNCFLVYEAENGSELLEWLFSES-SKTSNSVSVSLTWSQR	357
Query	413	ISMAVDVAMGLQYMHEAYPRIHRDITSSNILLDSNFKAKIANFSMARTFTNPMPKID I+A+DVA+GLQYMHEH YPRI+HRDIT+SNILL SNFKAKIANF MART TN MMPKID	472
Sbjct	358	ITIAMDVAIGLQYMHEHTYPRIIHRDITTSNILLGSNFKAKIANFGMARTSTNSMMPKID	417
Query	473	VFAFGVVLIELLTGRKAMTTKENGEVVMLWKDIWKIFDQEENREERLKKWMDPKLESYYP VFAFGVVLIELLTG+KAMTTKENGEVV+LWKD WKIFD E NEERL+KWMDPKLES+YP	532
Sbjct	418	VFAFGVVLIELLTGKAMTTKENGEVVLWKDFWKIFDLEGNRERLRKWMDPKLESFYP	477
Query	533	IDYALSLAS 541	
Sbjct	478	ID ALSLAS	
Sbjct	478	IDNALSLAS 486	

>emb|CAO02966.1| LysM-domain containing receptor-like kinase [Medicago tornata]
Length=487

Score = 741 bits (1914), Expect = 0.0, Method: Compositional matrix adjust.
Identities = 362/489 (74%), Positives = 414/489 (84%), Gaps = 4/489 (0%)

Query	54	YIAQSPNPLSLTNISNIFDTSPSLIARASNLEPMDDKLVKDQVLLPVTCGCTGNRSFAN Y AQSPPNPLSL+NIS++IF+SPL IA+ASN+E D KL+ DQ+LLPVTCGCT N SFAN	113
Sbjct	1	YRAQSPNPLSLNISDIFNLSPRLIAKASNIEADKKLIPDQLLVPVTCGCTKNHSFAN	60
Query	114	ISYEINQGDSFYFVATTSYENLNTWRAMDLNPVLPSPNKLPIGIQVVFPFLCKCPSKNQL I+Y I GD+F+ ++ TSY+NLTN+ + NP LSP LP+ +V PLFCCKCPSKNQL	173
Sbjct	61	ITYSIKLGDNFFSITSYQNLTNYLEFKNPNPNSPTLLPDTKVSVPFLCKCPSKNQL	120
Query	174	DKEIKYLITYVWKPGDNVLSQLDKFGASPEDIMSENNYQGNFTAANNLPLVLPVTRLPVL +K IKYLITYWV+ DNV+LVS KFGAS ++++ENN+ NFTA+ N VLIPTV LP L	233
Sbjct	121	NKGIKYLITYVWQDNDNVTLVSSKFGASQVEMLAENN--NFTASTNRNSVLPVTSPLPKL	178
Query	234	ARSPSDGRKGIR-LPVIIGISLGCTLLVLVLAFLVYVYCLMKTLNRSASSAETADKL + S+GRK + L +IIGISLG +LVL + LVVYVCLMK LNRS SS+ETADKL	292
Sbjct	179	DQPSNGRKSQQNLALIIGISAFFILVLTSLVYVYCLMKRKLNRSTSSSETADKL	238
Query	293	LSGVSGYVSKPTMYETDAIMEATMNLSEQCKIGESVYKANIEGKVLAVKRKFEDVTEELK LSGVSGYVSKPTMYE DAIME TMNL+S CKIGESVYKANI+G+VLAVK+ K+D +EELK	352
Sbjct	239	LSGVSGYVSKPTMYEIDAIMEGTMNLSDNCKIGESVYKANIDGRVLAVVKIKKDAEELK	298
Query	353	ILQKVNHNGLVKLMLGVSSDNDGNCFVVYEAENGSLDEWLFSKSCSDTSNSRASLTWCQR ILQKVNHNGLVKLMLGVSSDNDGNCF+VYEYAENGSL+EWLFS+S S TSNS SL+W QR	412
Sbjct	299	ILQKVNHNGLVKLMLGVSSDNDGNCFLVYEAENGSELLEWLFSES-SKTSNSVSVSLWSQR	357
Query	413	ISMAVDVAMGLQYMHEAYPRIHRDITSSNILLDSNFKAKIANFSMARTFTNPMPKID I+A+DVA+GLQYMHEH YPRI+HRDIT+SNILL SNFKAKIANF MART TN MMPKID	472
Sbjct	358	ITIAMDVAIGLQYMHEHTYPRIIHRDITTSNILLGSNFKAKIANFGMARTSTNSMMPKID	417
Query	473	VFAFGVVLIELLTGRKAMTTKENGEVVMLWKDIWKIFDQEENREERLKKWMDPKLESYYP VFAFGVVLIELLTG+KAMTTKENGEVV+LWKD WKIFD E NEERL+KWMDPKLES+YP	532
Sbjct	418	VFAFGVVLIELLTGKAMTTKENGEVVLWKDFWKIFDLEGNRERLRKWMDPKLESFYP	477
Query	533	IDYALSLAS 541	
Sbjct	478	ID ALSLAS	
Sbjct	478	IDNALSLAS 486	

>dbj|BAI79275.1| LysM type receptor kinase [Lotus japonicus]
dbj|BAI79285.1| LysM type receptor kinase [Lotus japonicus]
Length=591

GENE ID: 100380877 LYS11 | LysM type receptor kinase [Lotus japonicus]
(10 or fewer PubMed links)

Score = 704 bits (1817), Expect = 0.0, Method: Compositional matrix adjust.
Identities = 376/606 (62%), Positives = 461/606 (76%), Gaps = 23/606 (3%)

Query	1	MAVFFPFLPLHSQILCLVIMLFST--NIVAQSQQDNRTNFSCPSDSDPPSCETVVTYIAQS M FF F + + +M FST +I+AQ N TNFSCP DSPPSC+TVVTY AQS	58
Sbjct	1	MTSFFLFT---NTLFLA1MMFFSTTHHILAQLSHTNGTNFSCPVDSPPSCDTIVVTYFAQS	57
Query	59	PNFLSLTNISNIFDTSPSLIARASNLEPMDDKLVKDQVLLPVTCGCTGNRFANISYEI PNFL+LT+I+S++FDTSPLSLIARASN++ + LV Q+LLPVTC C+G+ SF+NIS+ I	118
Sbjct	58	PNFLTLTSISDLFDTSPLSLIARASNIDENQNLVPGQLLLVPVTCACSGSNFSNISHMI	117
Query	119	NQGDSFYFVATTSYENLNTWRAMDLNPVLPSPNKLPIGIQVVFPFLCKCPSKNQLDKEIK +G+S+Y++TTSYENLNTW V D NP +P LP+G+I+VV PLFCCKCP S L+K I+	178
Sbjct	118	KEGESYYLSTTSYENLNTWETVQDSNPNNPYLLPVPGIKVVIPLFCCKCPSNYHLNKIE	177
Query	179	YLITYVWKPGDNVLSDLKFGASPEDIMSENNY-QNFTAANNLPLVLPVTRLPVLARSP YLITYVW DNVSLV+ KFG S +DI+SENN+ QNFTAA N P+IPVT+LP L+I+S	237
Sbjct	178	YLITYVWHNNNDNVLVSAKFGVSTQDIISENNFSHQNFATAATNPFLIPVTQPLPSLSQSY	237
Query	238	SDGRKGGIIRLPVIIGISLGCTLLVLVLAFLVYVYCLMKM--TLNRSASSAETA-DKLL S + II L+ +A+L LV V CL+ + N+S S E A KL+ SSSERKRSNHIHIIISIGISLGSLLTALLVSVTCLRKRKSENKSLLSVEIAGKLL	293
Sbjct	238	SGVSGYVSKPTMYETDAIMEATMNLSEQCKIGESVYKANIEGKVLAVKRKFEDVTEELKI	353
Query	294	SGVSGYVSKPTMYETDAIMEATMNLSEQCKIGESVYKANIEGKVLAVKRKFEDVTEELKI SGVS YVSK +YE IMEAT+NL+EQCKIGESVYKA ++G+VLAVK+ KEDVTEEE+ I	353
Sbjct	298	SGVSNYVSKSILYEFRLIMEATLNLNQCKIGESVYKAKLDGQVLAVKKVEDVTEEVMI	357
Query	354	LQKVNHNGLVKLMLGVSSDNDGNCFVVYEAENGSLDEWLFSKSCSDTSNSRASLTWCRI LQKVNH NLVKLMLGVSS +DGN F+VYE+AENGSL WLFS S ++ SR LTW QRI	413
Sbjct	358	LQKVNHNGLVKLMLGVSSGHDGNHFLVYEAENGSLHNWLFSNS--STGSRF-LTWSQRI	413
Query	414	SMAVDVAMGLQYMHEAYPRIHRDITSSNILLDSNFKAKIANFSMARTFTNPMPKIDV S+AVDVAMGLQYMHEH P IVHRDITSSNILLDSNFKAKIANFS+ART NPM+ K+DV	473
Sbjct	414	SIAVDVAMGLQYMHEHTQPSIVHRDITSSNILLDSNFKAKIANFSVARTSINPMILKVDV	473
Query	474	FAFGVVLIELLTGRKAMTTKENGEVVMLWKDIWKIFDQEENREERLKKWMDPKLESYYP F+GVG+ELL+G+K+T N E+ I +IFD +E REER++WMDPK+ES YPI	533
Sbjct	474	FGYGVLLELLSGKKSLSL---NNEI---NHIREFIDLKKEERIRRWMDPKIESLYPI	526
Query	534	DYALSLASLAVNCTADKSLSRPTIAEIVLSSL-TQPSATLERSLTSSGLDVEATQIV D ALSLA LA+NCT++K LSRPT+ E+VLSLSS T Q SP TLERS T GLDV+ T++	592

Subjct 527 DDALSLAFLAMNCTSEKPLSRPTMGEVVLSLSLLMTQHSPTTLERSWT-CGLDVDVTEMQ 585

Query 593 TSIARAR 598

Subjct 586 TLIAAR 591

>gb|ADJ19109.1| truncated Nod-factor receptor 5A [Glycine max]
Length=337

Gene ID: 100498858 NFR5a | Nod-factor receptor 5A [Glycine max]
(10 or fewer PubMed links)

Score = 695 bits (1793), Expect = 0.0, Method: Compositional matrix adjust.
Identities = 337/337 (100%), Positives = 337/337 (100%), Gaps = 0/337 (0%)

Query 1 MAVFFPFLPLHSQILCLVIMLFSTNIVAQSQQDNRTNFSCPSDSSPPCETYVTYIAQSPN 60
MAVFFPFLPLHSQILCLVIMLFSTNIVAQSQQDNRTNFSCPSDSSPPCETYVTYIAQSPN
Subjct 1 MAVFFPFLPLHSQILCLVIMLFSTNIVAQSQQDNRTNFSCPSDSSPPCETYVTYIAQSPN 60

Query 61 FLSLTNISNIFDTSPLSIARASNLEPMDDKLVKDQVLLPVTCGCTGNRSFANISYEINQ 120
FLSLTNISNIFDTSPLSIARASNLEPMDDKLVKDQVLLPVTCGCTGNRSFANISYEINQ
Subjct 61 FLSLTNISNIFDTSPLSIARASNLEPMDDKLVKDQVLLPVTCGCTGNRSFANISYEINQ 120

Query 121 GDSFYFVATTSYENLTNWRRAVMDLNPVLSPNKLPIGIQVVFPLFCCKCPSKNQLDKEIKYL 180
GDSFYFVATTSYENLTNWRRAVMDLNPVLSPNKLPIGIQVVFPLFCCKCPSKNQLDKEIKYL
Subjct 121 GDSFYFVATTSYENLTNWRRAVMDLNPVLSPNKLPIGIQVVFPLFCCKCPSKNQLDKEIKYL 180

Query 181 ITYYWKGPDNVSLVSDKFGASPEDIMSENNYGGQNFTAANNLPVLIPVTRLPVLARSPSDG 240
ITYYWKGPDNVSLVSDKFGASPEDIMSENNYGGQNFTAANNLPVLIPVTRLPVLARSPSDG
Subjct 181 ITYYWKGPDNVSLVSDKFGASPEDIMSENNYGGQNFTAANNLPVLIPVTRLPVLARSPSDG 240

Query 241 RKGIGRLPVIIGISLGCTLLVLVLAVLLVYVYCLMKMTLNRSASSAETADKLLSGVSGYV 300
RKGIGRLPVIIGISLGCTLLVLVLAVLLVYVYCLMKMTLNRSASSAETADKLLSGVSGYV
Subjct 241 RKGIGRLPVIIGISLGCTLLVLVLAVLLVYVYCLMKMTLNRSASSAETADKLLSGVSGYV 300

Query 301 SKPTMYETDAIMEATMNLSEQCKIGESVYKANIEGKV 337
SKPTMYETDAIMEATMNLSEQCKIGESVYKANIEGKV
Subjct 301 SKPTMYETDAIMEATMNLSEQCKIGESVYKANIEGKV 337

>dbj|BAG85143.1| Nod factor receptor protein [Glycine soja]
dbj|BAG85149.1| Nod factor receptor protein [Glycine soja]
dbj|BAG85156.1| Nod factor receptor protein [Glycine soja]
11 more sequence titles

dbj|BAG85159.1| Nod factor receptor protein [Glycine max]
dbj|BAG85160.1| Nod factor receptor protein [Glycine max]
dbj|BAG85161.1| Nod factor receptor protein [Glycine max]
dbj|BAG85162.1| Nod factor receptor protein [Glycine max]
dbj|BAG85165.1| Nod factor receptor protein [Glycine max]
dbj|BAG85168.1| Nod factor receptor protein [Glycine max]
dbj|BAG85171.1| Nod factor receptor protein [Glycine max]
dbj|BAG85174.1| Nod factor receptor protein [Glycine max]
dbj|BAG85177.1| truncated Nod factor receptor protein [Glycine max]
dbj|BAG85179.1| Nod factor receptor protein [Glycine max]
dbj|BAG85180.1| Nod factor receptor protein [Glycine max]
Length=327

Score = 675 bits (1741), Expect = 0.0, Method: Compositional matrix adjust.
Identities = 327/327 (100%), Positives = 327/327 (100%), Gaps = 0/327 (0%)

Query 5 FPFPLPLHSQILCLVIMLFSTNIVAQSQQDNRTNFSCPSDSSPPCETYVTYIAQSPNFLSL 64
FPFPLPLHSQILCLVIMLFSTNIVAQSQQDNRTNFSCPSDSSPPCETYVTYIAQSPNFLSL
Subjct 1 FPFPLPLHSQILCLVIMLFSTNIVAQSQQDNRTNFSCPSDSSPPCETYVTYIAQSPNFLSL 60

Query 65 TNISNIFDTSPLSIARASNLEPMDDKLVKDQVLLPVTCGCTGNRSFANISYEINQGDSF 124
TNISNIFDTSPLSIARASNLEPMDDKLVKDQVLLPVTCGCTGNRSFANISYEINQGDSF
Subjct 61 TNISNIFDTSPLSIARASNLEPMDDKLVKDQVLLPVTCGCTGNRSFANISYEINQGDSF 120

Query 125 YFVATTSYENLTNWRRAVMDLNPVLSPNKLPIGIQVVFPLFCCKCPSKNQLDKEIKYLITYV 184
YFVATTSYENLTNWRRAVMDLNPVLSPNKLPIGIQVVFPLFCCKCPSKNQLDKEIKYLITYV
Subjct 121 YFVATTSYENLTNWRRAVMDLNPVLSPNKLPIGIQVVFPLFCCKCPSKNQLDKEIKYLITYV 180

Query 185 WKPGDNVSLVSDKFGASPEDIMSENNYGGQNFTAANNLPVLIPVTRLPVLARSPSDGRKGG 244
WKPGDNVSLVSDKFGASPEDIMSENNYGGQNFTAANNLPVLIPVTRLPVLARSPSDGRKGG
Subjct 181 WKPGDNVSLVSDKFGASPEDIMSENNYGGQNFTAANNLPVLIPVTRLPVLARSPSDGRKGG 240

Query 245 IRLPVIIGISLGCTLLVLVLAVLLVYVYCLMKMTLNRSASSAETADKLLSGVSGYVSKPT 304
IRLPVIIGISLGCTLLVLVLAVLLVYVYCLMKMTLNRSASSAETADKLLSGVSGYVSKPT
Subjct 241 IRLPVIIGISLGCTLLVLVLAVLLVYVYCLMKMTLNRSASSAETADKLLSGVSGYVSKPT 300

Query 305 MYETDAIMEATMNLSEQCKIGESVYKA 331
MYETDAIMEATMNLSEQCKIGESVYKA
Subjct 301 MYETDAIMEATMNLSEQCKIGESVYKA 327

>dbj|BAG85148.1| Nod factor receptor protein [Glycine soja]
Length=327

Score = 674 bits (1739), Expect = 0.0, Method: Compositional matrix adjust.
Identities = 326/327 (99%), Positives = 327/327 (100%), Gaps = 0/327 (0%)

Query 5 FPFPLPLHSQILCLVIMLFSTNIVAQSQQDNRTNFSCPSDSSPPCETYVTYIAQSPNFLSL 64
FPFPLPLHSQILCLVIMLFSTNIVAQSQQDNRTNFSCPSDSSPPCETYVTYIAQSPNFLSL
Subjct 1 FPFPLPLHSQILCLVIMLFSTNIVAQSQQDNRTNFSCPSDSSPPCETYVTYIAQSPNFLSL 60

Query 65 TNISNIFDTSPLSIARASNLEPMDDKLVKDQVLLPVTCGCTGNRSFANISYEINQGDSF 124
TNISNIFDTSPLSIARASNLEPMDDKLVKDQVLLPVTCGCTGNRSFANISYEINQGDSF
Subjct 61 TNISNIFDTSPLSIARASNLEPMDDKLVKDQVLLPVTCGCTGNRSFANISYEINQGDSF 120

Query 125 YFVATTSYENLTNWRRAVMDLNPVLSPNKLPIGIQVVFPLFCCKCPSKNQLDKEIKYLITYV 184
YFVATTSYENLTNWRRAVMDLNPVLSPNKLPIGIQVVFPLFCCKCPSKNQLDKEIKYLITYV
Subjct 121 YFVATTSYENLTNWRRAVMDLNPVLSPNKLPIGIQVVFPLFCCKCPSKNQLDKEIKYLITYV 180

Query 185 WKPGDNVSLVSDKFGASPEDIMSENNYGGQNFTAANNLPVLIPVTRLPVLARSPSDGRKGG 244
WKPGDNVSLVSDKFGASPEDIMSENNYGGQNFTAANNLPVLIPVTRLPVLARSPSDGRKGG
Subjct 181 WKPGDNVSLVSDKFGASPEDIMSENNYGGQNFTAANNLPVLIPVTRLPVLARSPSDGRKGG 240

Sbjct	181	WKPGDNVLVSDKFGASPEDIMSENNYQNFATAANLPLVLPVTRLPVLARSPSDGRKG	240
Query	245	IRLPVIIIGISLGCTLLVLVLAVLVLVVYVYCLKMKTLNRSASSAETADKLLSGVSGYVSKPT	304
		IRLPVIIIGISLGCTLLVLVLAVLVLVVYVYCLKMKTLNRSASSAETADKLLSGVSGYVSKPT	
Sbjct	241	IRLPVIIIGISLGCTLLVLVLAVLVLVVYVYCLKMKTLNRSASSAETADKLLSGVSGYVSKPT	300
Query	305	MYETDAIMEATMNLSEQCCKIGESVYKA 331	
Sbjct	301	MYETDAIMEATMNLSEQCCKIGESVYKA 327	

>dbj|BAG85151.1| Nod factor receptor protein [Glycine soja]
Length=327

Score = 673 bits (1736), Expect = 0.0, Method: Compositional matrix adjust.
Identities = 326/327 (99%), Positives = 327/327 (100%), Gaps = 0/327 (0%)

Query	5	FPFLPLHSQLCLCIVMLFSTNIVAQSQQDNRTNFSCPSDPPSCETYVTYIAQSPNFLSL	64
Sbjct	1	FPFLPLHSQLCLCIVMLFSTNIVAQSQQDNRTNFSCPSDPPSCETYVTYIAQSPNFLSL	60
Query	65	TNISNI FDTPLS LSTARAS NLE PMD KLV D KV D QV L L V P V T C G C T G N R S F A N I S Y E I N Q G D S F	124
Sbjct	61	TNISNI FETPSL STARAS NLE PMD KLV D KV D QV L L V P V T C G C T G N R S F A N I S Y E I N Q G D S F	120
Query	125	YFVATT SYEN LTNRW A M V D L N P V L S P N K L P I G I Q V W F P L E C K C P S K N Q L D K E I K Y L I T Y V	184
Sbjct	121	YFVATT SYEN LTNRW A M V D L N P V L S P N K L P I G I Q V W F P L E C K C P S K N Q L D K E I K Y L I T Y V	180
Query	185	WKPGDNVSLVSDKF GAS PEDIM SEN NYG Q N FTA ANN LP VL I P V T R L P V L A R S P S D G R K G G	244
Sbjct	181	WKPGDNVSLVSDKF GAS PEDIM SEN NYG Q N FTA ANN LP VL I P V T R L P V L A R S P S D G R K G G	240
Query	245	I RLPVIIGISLGCTLLVLVLAVLLVVYCLKMTKLNRSSAETADKLLSGVGSGYVSKPT	304
Sbjct	241	I RLPVIIGISLGCTLLVLVLAVLLVVYCLKMTKLNRSSAETADKLLSGVGSGYVSKPT	300
Query	305	MYETDAIMEATMNLSEQCKIGESVYKA 331	
Sbjct	301	MYETDAIMEATMNLSEQCKIGESVYKA 327	

>dbj|BAG85178.1| Nod factor receptor protein [Glycine max]
Length=327

GENE ID: 100498858 NFR5a | Nod-factor receptor 5A [Glycine max] (10 or fewer PubMed links)

Score	=	673 bits (1736),	Expect	=	0.0,	Method:	Compositional matrix adjust.
Identities	=	326/327 (99%),	Positives	=	327/327 (100%),	Gaps	= 0/327 (0%)
Query	5	FPFLPLHSQILCLVIMLFNSTNIVAQSQQDNRTNFSCPSDSSPPSCETYVTYIAQSPNFLSL					64
Sbjct	1	FPFLPLHSQILCLVIMLFNSTNIVAQSQQDNRTNFSCPSDSSPPSCETYVTYIAQSPNFLSL					60
Query	65	TNISNIFDTSPLSIARASNLEPMDDKLVKDQVLLPVTCGCTGNRSFANISYEINQGDSF					124
Sbjct	61	TNISNIFDTPLSIARASNLEPMDDKLVKDQVLLPVTCGCTGNRSFANISYEINQGDSF					120
Query	125	YFVATTSYENLTNWRAVMDLNPVLSPNKLPIGIQVVFPLFCPKCPSKNQLDKEIKYLITYV					184
Sbjct	121	YFVATTSYENLTNWRAVMDLNPVLSPNKLPIGIQVVFPLFCPKCPSKNQLDKEIKYLITYV					180
Query	185	WKPGDNVSLVSDKFGASEPEDIMSENNYQGNFTAANNLPVLIPVTRLPVLARSPSDGRKGG					244
Sbjct	181	WKPGDNVSLVSDKFGASEPEDIMSENNYQGNFTAANNLPVLIPVTRLPVLARSPSDGRKGG					240
Query	245	IRLPVIIGISLGCTLLVLVLAVLLVVYCLRMKTLNRSASSAETADKLLSGVSGYVSKPT					304
Sbjct	241	IRLPVIIGISLGCTLLVLVLAVLLVVYCLRMKTLNRSASSAETADKLLSGVSGYVSKPT					300
Query	305	MYETDAIMEATMNLSEQCKIGESVYKA	331				
Sbjct	301	MYETDAIMEATMNLSEQCKIGESVYKA	327				

>dbj|BAG85167.1| Nod factor receptor protein [Glycine max]
Length=327

Score = 673 bits (1736), Expect = 0.0, Method: Compositional matrix adjust.
Identities = 326/327 (99%), Positives = 326/327 (99%), Gaps = 0/327 (0%)

Query	5	FPFLPLHSQLCLCIVMLFSTNIVAQSQQDNRTNFSCPSDPPSCETYVYTYIAQSPNFLSL	64
Sbjct	1	FPFLPLHSQLCLCIVMLFSTNIVAQSQQDNRTNFSCPSDPPSCETYVYTYIAQSPNFLSL	60
Query	65	TNISNIFDTSPLSIARASNLPEMDDKLVKDQVLVPVTCGCTGNRSFANISYEINQGDSF	124
Sbjct	61	NISNIFDTSPLSIARASNLPEMDDKLVKDQVLVPVTCGCTGNRSFANISYEINQGDSF	120
Query	125	YFVATTSYENLTNWRAVMDLNPVLSPNKLPIGIQVVFPLFCCKCPSKNQLDKEIKYLITYV	184
Sbjct	121	YFVATTSYENLTNWRAVMDLNPVLSPNKLPIGIQVVFPLFCCKCPSKNQLDKEIKYLITYV	180
Query	185	WKPGDNVSLVSDKGASPEDIMSENNYGQNFTAANNLVLIPVTRLPVLARSPSDGRGG	244
Sbjct	181	WKPGDNVSLVSDKGASPEDIMSENYYGQNFTAANNLVLIPVTRLPVLARSPSDGRGG	240
Query	245	IRLPVIIGISLGCTLLVLVLAVLLVVYCLKMTLNRSASSAETADKLLSGVGSGYVSKPT	304
Sbjct	241	IRLPVIIGISLGCTLLVLVLAVLLVVYCLKMTLNRSASSAETADKLLSGVGSGYVSKPT	300
Query	305	MYETDAIMEATMNLSEQCKIGESVYKA 331	
Sbjct	301	MYETDAIMEATMNLSEQCKIGESVYKA 327	

>dbj|BAG85164.1| Nod factor receptor protein [Glycine max]
Length=327

Score = 673 bits (1736), Expect = 0.0, Method: Compositional matrix adjust.
Identities = 326/327 (99%), Positives = 326/327 (99%), Gaps = 0/327 (0%)

Query 5	FPFLPLHSQILCLVIMLFLSTNIVAQSQQDNRTNFSCPSDSDPSCPSETYVTYIAQSPNFLSL	64
Sbjct 1	FPFLPLHSQILCLVIMLFLSTNIVAQSQQDNRTNFSCPSDSDPSCPSETYVTYIAQSPNFLSL	60
Query 65	TNISNIFDTSPSLSIARASNLEPMDDKLVKDQVLLVPVTCGCTGNRSFANISYEINQGDSF	124
Sbjct 61	TNISNIFDTSPSLSIARASNLEPMDDKLVKDQVLLVPVTCGCTGNRSFANISYEINQGDSF	120
Query 125	YFVATTTSYENLTNRAVMDLNPVLSPNKLPIGIQVVVFPLFCCKCPSKNQLDKEIKYLITYV	184
Sbjct 121	YFVATTTSYENLTNRAVMDLNPVLSPNKLPIGIQVVVFPLFCCKCPSKNQLDKEIKYLITYV	180
Query 185	WKGDNVSLVSDKFGASPEDIMSENNYQGNFTAANNLPVLIPVTRLPVLARSPSDGRKGG	244
Sbjct 181	WKGDNVSLVSDKFGASPEDIMSENNYQGNFTAANNLPVLIPVTRLPVLARSPSDGRKGG	240
Query 245	IRLPVIIIGISLGCTLLVLVLAVILLVYVYCLMKTLNRSASSAETADKLLSGVSGYVSKPT	304
Sbjct 241	IRLPVIIIGISLGCTLLVLVLAVILLVYVYCLMKTLNRSASSAETADKLLSGVSGYVSKPT	300
Query 305	MYETDAIMEATMNLSEQCKIGESVYKA 331	
Sbjct 301	MYETDAIMEATMNLSEQCKIGESVYKA 327	

>dbj|BAG85170.1| Nod factor receptor protein [Glycine max]
Length=327

Score = 672 bits (1735), Expect = 0.0, Method: Compositional matrix adjust.
Identities = 326/327 (99%), Positives = 327/327 (100%), Gaps = 0/327 (0%)

Query 5	FPFLPLHSQILCLVIMLFLSTNIVAQSQQDNRTNFSCPSDSDPSCPSETYVTYIAQSPNFLSL	64
Sbjct 1	FPFLPLHSQILCLVIMLFLSTNIVAQSQQDNRTNFSCPSDSDPSCPSETYVTYIAQSPNFLSL	60
Query 65	TNISNIFDTSPSLSIARASNLEPMDDKLVKDQVLLVPVTCGCTGNRSFANISYEINQGDSF	124
Sbjct 61	TNISNIFDTSPSLSIARASNLEPMDDKLVKDQVLLVPVTCGCTGNRSFA+ISYEINQGDSF	120
Query 125	YFVATTTSYENLTNRAVMDLNPVLSPNKLPIGIQVVVFPLFCCKCPSKNQLDKEIKYLITYV	184
Sbjct 121	YFVATTTSYENLTNRAVMDLNPVLSPNKLPIGIQVVVFPLFCCKCPSKNQLDKEIKYLITYV	180
Query 185	WKGDNVSLVSDKFGASPEDIMSENNYQGNFTAANNLPVLIPVTRLPVLARSPSDGRKGG	244
Sbjct 181	WKGDNVSLVSDKFGASPEDIMSENNYQGNFTAANNLPVLIPVTRLPVLARSPSDGRKGG	240
Query 245	IRLPVIIIGISLGCTLLVLVLAVILLVYVYCLMKTLNRSASSAETADKLLSGVSGYVSKPT	304
Sbjct 241	IRLPVIIIGISLGCTLLVLVLAVILLVYVYCLMKTLNRSASSAETADKLLSGVSGYVSKPT	300
Query 305	MYETDAIMEATMNLSEQCKIGESVYKA 331	
Sbjct 301	MYETDAIMEATMNLSEQCKIGESVYKA 327	

>dbj|BAG85146.1| Nod factor receptor protein [Glycine soja]
Length=327

Score = 672 bits (1735), Expect = 0.0, Method: Compositional matrix adjust.
Identities = 326/327 (99%), Positives = 327/327 (100%), Gaps = 0/327 (0%)

Query 5	FPFLPLHSQILCLVIMLFLSTNIVAQSQQDNRTNFSCPSDSDPSCPSETYVTYIAQSPNFLSL	64
Sbjct 1	FPFLPLHSQILCLVIMLFLSTNIVAQSQQDNRTNFSCPSDSDPSCPSETYVTYIAQSPNFLSL	60
Query 65	TNISNIFDTSPSLSIARASNLEPMDDKLVKDQVLLVPVTCGCTGNRSFANISYEINQGDSF	124
Sbjct 61	TNISNIFDTSPSLSIARASNLEPMDDKLVKDQVLLVPVTCGCTGNRSFANISYEINQGDSF	120
Query 125	YFVATTTSYENLTNRAVMDLNPVLSPNKLPIGIQVVVFPLFCCKCPSKNQLDKEIKYLITYV	184
Sbjct 121	YFVATTTSYENLTNRAVMDLNPVLSPNKLPIGIQVVVFPLFCCKCPSKNQLDKEIKYLITYV	180
Query 185	WKGDNVSLVSDKFGASPEDIMSENNYQGNFTAANNLPVLIPVTRLPVLARSPSDGRKGG	244
Sbjct 181	WKGDNVSLVSDKFGASPEDIMSENNYQGNFTAANNLPVLIPVTRLPVLARSPSDGRKGG	240
Query 245	IRLPVIIIGISLGCTLLVLVLAVILLVYVYCLMKTLNRSASSAETADKLLSGVSGYVSKPT	304
Sbjct 241	IRLPVIIIGISLGCTLLVLVLAVILLVYVYCLMKTLNRSASSAETADKLLSGVSGYVSKPT	300
Query 305	MYETDAIMEATMNLSEQCKIGESVYKA 331	
Sbjct 301	MYETDAIMEATMNLSEQCKIGESVYKA 327	

>dbj|BAG85158.1| Nod factor receptor protein [Glycine max]
Length=327

GENE ID: 100301877 nfr5a | Nod factor receptor protein [Glycine max]
(10 or fewer PubMed links)

Score = 672 bits (1735), Expect = 0.0, Method: Compositional matrix adjust.
Identities = 326/327 (99%), Positives = 326/327 (99%), Gaps = 0/327 (0%)

Query 5	FPFLPLHSQILCLVIMLFLSTNIVAQSQQDNRTNFSCPSDSDPSCPSETYVTYIAQSPNFLSL	64
Sbjct 1	FPFLPLHSQILCLVIMLFLSTNIVAQSQQDNRTNFSCPSDSDPSCPSETYVTYIAQSPNFLSL	60
Query 65	TNISNIFDTSPSLSIARASNLEPMDDKLVKDQVLLVPVTCGCTGNRSFANISYEINQGDSF	124

Sbjct	61	TNISNIFDTSPLSIARASNLEPMDDKLVQDQVLLVPVTCGCTGNRSFANISYEINQGDSF TNISNIFDTSPLSIARASNLEPMDDKLVQDQVLLVPVTCGCTGNRSFANISYEINQGDSF	120
Query	125	YFVATTSYENLTNWRAVMMDLNPLSPNPKLPIGIQVVFPFLCKCPSKNQLDKEIKYLITYV YFVATTSYENLTNWRAVMMDLNPLSPNPKLPIGIQVVFPFLCKCPSKNQLDKEIKYLITYV	184
Sbjct	121	YFVATTSYENLTNWRAVMMDLNPLSPNPKLPIGIQVVFPFLCKCPSKNQLDKEIKYLITYV	180
Query	185	WKGPDNVSLVSDKFGASPEDIMSENNYQGNFTAANNLPVLIPVTRLPVLARSPSDGRKGG WKGPDNVSLVSDKFGASPEDIMSENNYQGNFTAANNLPVLIPVTRLPVLARSPSDGRKGG	244
Sbjct	181	WKGPDNVSLVSDKFGASPEDIMSENNYQGNFTAANNLPVLIPVTRLPVLARSPSDGRKGG WKGPDNVSLVSDKFGASPEDIMSENNYQGNFTAANNLPVLIPVTRLPVLARSPSDGRKGG	240
Query	245	IRLPVIIIGISLGCTLLVLVLAVLILVVYVYCLKMKTLNRSASSAETADKLLSGVSGYVSKPT IRLPVIIIGISLGCTLLVLVLAVLILVVYVYCLKMKTLNRSASSAETADKLLSGVSGYVSKPT	304
Sbjct	241	IRLPVIIIGISLGCTLLVLVLAVLILVVYVYCLKMKTLNRSASSAETADKLLSGVSGYVSKPT IRLPVIIIGISLGCTLLVLVLAVLILVVYVYCLKMKTLNRSASSAETADKLLSGVSGYVSKPT	300
Query	305	MYETDAIMEATMNLSEQCKIGESVYKA 331	
Sbjct	301	MYETDAIMEATMNLSEQCKIGESVYKA 327	

>**dbj|BAG85144.1| Nod factor receptor protein [Glycine soja]**
dbj|BAG85145.1| Nod factor receptor protein [Glycine soja]
Length=327

Score = 672 bits (1734), Expect = 0.0, Method: Compositional matrix adjust.
Identities = 326/327 (99%), Positives = 326/327 (99%), Gaps = 0/327 (0%)

Query	5	FPFLPLHSQILC1VIMLFSTNIVAQSQQDNRTNFSCPSDSSPCSETYVTYIAQSPNFLSL FPFLPLH Q1LC1VIMLFSTNIVAQSQQDNRTNFSCPSDSSPCSETYVTYIAQSPNFLSL	64
Sbjct	1	FPFLPLHFQ1LC1VIMLFSTNIVAQSQQDNRTNFSCPSDSSPCSETYVTYIAQSPNFLSL	60
Query	65	TNISNIFDTSPLSIARASNLEPMDDKLVQDQVLLVPVTCGCTGNRSFANISYEINQGDSF TNISNIFDTSPLSIARASNLEPMDDKLVQDQVLLVPVTCGCTGNRSFANISYEINQGDSF	124
Sbjct	61	TNISNIFDTSPLSIARASNLEPMDDKLVQDQVLLVPVTCGCTGNRSFANISYEINQGDSF TNISNIFDTSPLSIARASNLEPMDDKLVQDQVLLVPVTCGCTGNRSFANISYEINQGDSF	120
Query	125	YFVATTSYENLTNWRAVMMDLNPLSPNPKLPIGIQVVFPFLCKCPSKNQLDKEIKYLITYV YFVATTSYENLTNWRAVMMDLNPLSPNPKLPIGIQVVFPFLCKCPSKNQLDKEIKYLITYV	184
Sbjct	121	YFVATTSYENLTNWRAVMMDLNPLSPNPKLPIGIQVVFPFLCKCPSKNQLDKEIKYLITYV	180
Query	185	WKGPDNVSLVSDKFGASPEDIMSENNYQGNFTAANNLPVLIPVTRLPVLARSPSDGRKGG WKGPDNVSLVSDKFGASPEDIMSENNYQGNFTAANNLPVLIPVTRLPVLARSPSDGRKGG	244
Sbjct	181	WKGPDNVSLVSDKFGASPEDIMSENNYQGNFTAANNLPVLIPVTRLPVLARSPSDGRKGG WKGPDNVSLVSDKFGASPEDIMSENNYQGNFTAANNLPVLIPVTRLPVLARSPSDGRKGG	240
Query	245	IRLPVIIIGISLGCTLLVLVLAVLILVVYVYCLKMKTLNRSASSAETADKLLSGVSGYVSKPT IRLPVIIIGISLGCTLLVLVLAVLILVVYVYCLKMKTLNRSASSAETADKLLSGVSGYVSKPT	304
Sbjct	241	IRLPVIIIGISLGCTLLVLVLAVLILVVYVYCLKMKTLNRSASSAETADKLLSGVSGYVSKPT IRLPVIIIGISLGCTLLVLVLAVLILVVYVYCLKMKTLNRSASSAETADKLLSGVSGYVSKPT	300
Query	305	MYETDAIMEATMNLSEQCKIGESVYKA 331	
Sbjct	301	MYETDAIMEATMNLSEQCKIGESVYKA 327	

>**dbj|BAG85142.1| Nod factor receptor protein [Glycine soja]**
Length=327

Score = 672 bits (1734), Expect = 0.0, Method: Compositional matrix adjust.
Identities = 326/327 (99%), Positives = 326/327 (99%), Gaps = 0/327 (0%)

Query	5	FPFLPLHSQILC1VIMLFSTNIVAQSQQDNRTNFSCPSDSSPCSETYVTYIAQSPNFLSL FPFLPLHSQILC1VIMLFSTNIVAQSQQDNRTNFSCPSDSSPCSETYVTYIAQSPNFLSL	64
Sbjct	1	FPFLPLHSQILC1VIMLFSTNIVAQSQQDNRTNFSCPSDSSPCSETYVTYIAQSPNFLSL	60
Query	65	TNISNIFDTSPLSIARASNLEPMDDKLVQDQVLLVPVTCGCTGNRSFANISYEINQGDSF TNISNIFDTSPLSIARASNLEPMDDKLVQDQVLLVPVTCGCTGNRSFANISYEINQGDSF	124
Sbjct	61	TNISNIFDTSPLSIARASNLEPMDDKLVQDQVLLVPVTCGCTGNRSFANISYEINQGDSF TNISNIFDTSPLSIARASNLEPMDDKLVQDQVLLVPVTCGCTGNRSFANISYEINQGDSF	120
Query	125	YFVATTSYENLTNWRAVMMDLNPLSPNPKLPIGIQVVFPFLCKCP SKNQLDKEIKYLITYV YFVATTSYENLTNWRAVMMDLNPLSPNPKLPIGIQVVFPFLCKCP SKNQLDKEIKYLITYV	184
Sbjct	121	YFVATTSYENLTNWRAVMMDLNPLSPNPKLPIGIQVVFPFLCKCP SKNQLDKEIKYLITYV	180
Query	185	WKGPDNVSLVSDKFGASPEDIMSENNYQGNFTAANNLPVLIPVTRLPVLARSPSDGRKGG WKGPDNV LVSDKFGASPEDIMSENNYQGNFTAANNLPVLIPVTRLPVLARSPSDGRKGG	244
Sbjct	181	WKGPDNVFLVSDKFGASPEDIMSENNYQGNFTAANNLPVLIPVTRLPVLARSPSDGRKGG WKGPDNVFLVSDKFGASPEDIMSENNYQGNFTAANNLPVLIPVTRLPVLARSPSDGRKGG	240
Query	245	IRLPVIIIGISLGCTLLVLVLAVLILVVYVYCLKMKTLNRSASSAETADKLLSGVSGYVSKPT IRLPVIIIGISLGCTLLVLVLAVLILVVYVYCLKMKTLNRSASSAETADKLLSGVSGYVSKPT	304
Sbjct	241	IRLPVIIIGISLGCTLLVLVLAVLILVVYVYCLKMKTLNRSASSAETADKLLSGVSGYVSKPT IRLPVIIIGISLGCTLLVLVLAVLILVVYVYCLKMKTLNRSASSAETADKLLSGVSGYVSKPT	300
Query	305	MYETDAIMEATMNLSEQCKIGESVYKA 331	
Sbjct	301	MYETDAIMEATMNLSEQCKIGESVYKA 327	

>**dbj|BAG85152.1| Nod factor receptor protein [Glycine soja]**
Length=327

Score = 672 bits (1733), Expect = 0.0, Method: Compositional matrix adjust.
Identities = 326/327 (99%), Positives = 326/327 (99%), Gaps = 0/327 (0%)

Query	5	FPFLPLHSQILC1VIMLFSTNIVAQSQQDNRTNFSCPSDSSPCSETYVTYIAQSPNFLSL FPFLPLHSQILC1VIMLFSTNIVAQSQQDNRTNFSCPSDSSPCSETYVTYIAQSPNFLSL	64
Sbjct	1	FPFLPLHSQILC1VIMLFSTNIVAQSQQDNRTNFSCPSDSSPCSETYVTYIAQSPNFLSL	60
Query	65	TNISNIFDTSPLSIARASNLEPMDDKLVQDQVLLVPVTCGCTGNRSFANISYEINQGDSF TNISNIFDTSPLSIARASNLEPMDDKLVQDQVLLVPVTCGCTGNRSFANISYEINQGDSF	124
Sbjct	61	TNISNIFDTSPLSIARASNLEPMDDKLVQDQVLLVPVTCGCTGNRSFANISYEINQGDSF TNISNIFDTSPLSIARASNLEPMDDKLVQDQVLLVPVTCGCTGNRSFANISYEINQGDSF	120
Query	125	YFVATTSYENLTNWRAVMMDLNPLSPNPKLPIGIQVVFPFLCKCP SKNQLDKEIKYLITYV YFVATTSYENLTNWRAVMMDLNPLSPNPKLPIGIQVVFPFLCKCP SKNQLDKEIKYLITYV	184
Sbjct	121	YFVATTSYENLTNWRAVMMDLNPLSPNPKLPIGIQVVFPFLCKCP SKNQLDKEIKYLITYV	180
Query	185	WKGPDNVSLVSDKFGASPEDIMSENNYQGNFTAANNLPVLIPVTRLPVLARSPSDGRKGG WKGPDNV SLVSDKFGASPEDIMSENNYQGNFTAANNLPVLIPVTRLPVLARSPSDGRKGG	244
Sbjct	181	WKGPDNVSLVSDKFGASPEDIMSENNYQGNFTAANNLPVLIPVTRLPVLARSPSDGRKGG WKGPDNVSLVSDKFGASPEDIMSENNYQGNFTAANNLPVLIPVTRLPVLARSPSDGRKGG	240
Query	245	IRLPVIIIGISLGCTLLVLVLAVLILVVYVYCLKMKTLNRSASSAETADKLLSGVSGYVSKPT IRLPVIIIGISLGCTLLVLVLAVLILVVYVYCLKMKTLNRSASSAETADKLLSGVSGYVSKPT	304
Sbjct	241	IRLPVIIIGISLGCTLLVLVLAVLILVVYVYCLKMKTLNRSASSAETADKLLSGVSGYVSKPT IRLPVIIIGISLGCTLLVLVLAVLILVVYVYCLKMKTLNRSASSAETADKLLSGVSGYVSKPT	300

Query 305 MYETDAIMEATMNLSEQCKIGESVYKA 331
 Sbjct 301 MYETDAIMEATMNLSEQCKIGESVYKA 327

>dbj|BAG85175.1| Nod factor receptor protein [Glycine max]
 Length=327

Score = 672 bits (1733), Expect = 0.0, Method: Compositional matrix adjust.
 Identities = 325/327 (99%), Positives = 326/327 (99%), Gaps = 0/327 (0%)

Query 5	FPPFLPLHSQILC1LVIMLFSTNIVAQSQQDNRTNFSCPSDSSPCSETYVTYIAQSPNFLSL	64
Sbjct 1	FPPFLPLHSQILC1LVIMLFSTNIVAQSQQDNRTNFSCPSDSSPCSETYVTYIAQSPNFLSL	60
Query 65	TNISNIFDTSPSLSIARASNLPEPMDKLVKDQVLLVPVTCGCTGNRSFANISYEINQGDSF	124
Sbjct 61	TNISNIFDTSPSLSIARASNLPEPMDKLVKDQVLLVPVTCGCTGNRSFANISYEINQGDSF	120
Query 125	YFVATTSYENLTNWRAVMDLNPVLSPNKLPIGIQVVFPFLFCPKCPSKNQLDKEIKYLITYV	184
Sbjct 121	YFVATTSYENLTNWRAVMDLNPVLSPNKLPIGIQVVFPFLFCPKCPSKNQLDKEIKYLITYV	180
Query 185	WKGPDNVSLVSDKFGASPEDIMSENNYQGNFTAANNLPVLIPVTRLPVLARSPSDGRKGG	244
Sbjct 181	WKGPDNVSLVSDKFGASPEDIMSENNYQGNFTAANNLPVLIPVTRLPVLARSPSDGRKGG	240
Query 245	IRLPVIIGISLGCTLLVLVLAVLLVYVYCLMKTLNRASSAETADKLLSGVSGYVSKPT	304
Sbjct 241	IRLPVIIGISLGCTLLVLVLAVLLVYVYCLMKTLNRASSAETADKLLSGVSGYVSKPT	300
Query 305	MYETDAIMEATMNLSEQCKIGESVYKA 331	
Sbjct 301	MYETDAIMEATMNLSEQCKIGESVYKA 327	

>dbj|BAG85172.1| Nod factor receptor protein [Glycine max]
 Length=327

Score = 671 bits (1732), Expect = 0.0, Method: Compositional matrix adjust.
 Identities = 326/327 (99%), Positives = 326/327 (99%), Gaps = 0/327 (0%)

Query 5	FPPFLPLHSQILC1LVIMLFSTNIVAQSQQDNRTNFSCPSDSSPCSETYVTYIAQSPNFLSL	64
Sbjct 1	FPPFLPLHSQILC1LVIMLFSTNIVAQSQQDNRTNFSCPSDSSPCSETYVTYIAQSPNFLSL	60
Query 65	TNISNIFDTSPSLSIARASNLPEPMDKLVKDQVLLVPVTCGCTGNRSFANISYEINQGDSF	124
Sbjct 61	TNISNIFDTSPSLSIARASNLPEPMDKLVKDQVLLVPVTCGCTGNRSFANISYEINQGDSF	120
Query 125	YFVATTSYENLTNWRAVMDLNPVLSPNKLPIGIQVVFPFLFCPKCPSKNQLDKEIKYLITYV	184
Sbjct 121	YFVATTSYENLTNWRAVMDLNPVLSPNKLPIGIQVVFPFLFCPKCPSKNQLDKEIKYLITYV	180
Query 185	WKGPDNVSLVSDKFGASPEDIMSENNYQGNFTAANNLPVLIPVTRLPVLARSPSDGRKGG	244
Sbjct 181	WKGPDNVSLVSDKFGASPEDIMSENNYQGNFTAANNLPVLIPVTRLPVLARSPSDGRKGG	240
Query 245	IRLPVIIGISLGCTLLVLVLAVLLVYVYCLMKTLNRASSAETADKLLSGVSGYVSKPT	304
Sbjct 241	IRLPVIIGISLGCTLLVLVLAVLLVYVYCLMKTLNRASSAETADKLLSGVSGYVSKPT	300
Query 305	MYETDAIMEATMNLSEQCKIGESVYKA 331	
Sbjct 301	MYETDAIMEATMNLSEQCKIGESVYKA 327	

>dbj|BAG85157.1| Nod factor receptor protein [Glycine soja]
 Length=327

Score = 671 bits (1732), Expect = 0.0, Method: Compositional matrix adjust.
 Identities = 326/327 (99%), Positives = 326/327 (99%), Gaps = 0/327 (0%)

Query 5	FPPFLPLHSQILC1LVIMLFSTNIVAQSQQDNRTNFSCPSDSSPCSETYVTYIAQSPNFLSL	64
Sbjct 1	FPPFLPLHSQILC1LVIMLFSTNIVAQSQQDNRTNFSCPSDSSPCSETYVTYIAQSPNFLSL	60
Query 65	TNISNIFDTSPSLSIARASNLPEPMDKLVKDQVLLVPVTCGCTGNRSFANISYEINQGDSF	124
Sbjct 61	TNISNIFDTSPSLSIARASNLPEPMDKLVKDQVLLVPVTCGCTGNRSFANISYEINQGDSF	120
Query 125	YFVATTSYENLTNWRAVMDLNPVLSPNKLPIGIQVVFPFLFCPKCPSKNQLDKEIKYLITYV	184
Sbjct 121	YFVATTSYENLTNWRAVMDLNPVLSPNKLPIGIQVVFPFLFCPKCPSKNQLDKEIKYLITYV	180
Query 185	WKGPDNVSLVSDKFGASPEDIMSENNYQGNFTAANNLPVLIPVTRLPVLARSPSDGRKGG	244
Sbjct 181	WKGPDNVSLVSDKFGASPEDIMSENNYQGNFTAANNLPVLIPVTRLPVLARSPSDGRKGG	240
Query 245	IRLPVIIGISLGCTLLVLVLAVLLVYVYCLMKTLNRASSAETADKLLSGVSGYVSKPT	304
Sbjct 241	IRLPVIIGISLGCTLLVLVLAVLLVYVYCLMKTLNRASSAETADKLLSGVSGYVSKPT	300
Query 305	MYETDAIMEATMNLSEQCKIGESVYKA 331	
Sbjct 301	MYETDAIMEATMNLSEQCKIGESVYKA 327	

>dbj|BAG85150.1| Nod factor receptor protein [Glycine soja]
 Length=327

Score = 671 bits (1731), Expect = 0.0, Method: Compositional matrix adjust.
 Identities = 325/327 (99%), Positives = 325/327 (99%), Gaps = 0/327 (0%)

Query 5	FPPFLPLHSQILC1LVIMLFSTNIVAQSQQDNRTNFSCPSDSSPCSETYVTYIAQSPNFLSL	64
Sbjct 1	FPPFLPLHSQILC1LVIMLFSTNIVAQSQQDNRTNFSCPSDSSPCSETYVTYIAQSPNFLSL	60

Query 65 TNISNIFDTSPSLSIARASNLLEPMDDKLVQDQVLLVPVTCGCTGNRSFANISYEINQGDSF 124
 Sbjct 61 TNISNIFDTSPSLSIARASNLLEPMDDKLVQDQVLLVPVTCGCTGNRSFANISYEINQGDSF 120

Query 125 YFVATTSYENLTNWRAVMDLNPVLSPNPKLPIGIQVVFPLFCCKCPSKNQLDKEIKYLITYV 184
 Sbjct 121 YFVATTSYENLTNWRAVMDLNPVLSPNPKLPIGIQVVFPLFCCKCPSKNQLDKEIKYLITYV 180

Query 185 WKGDNVSLVSDKFGASPEDIMSENNYQONFTAANNLPVLIPVTRLPVLARSPSDGRKGG 244
 Sbjct 181 WKGDNVSLVSDKFGASPEDIMSENNYQONFTAANNLPVLIPVTRLPVLARSPSDGRKGG 240

Query 245 IRLPVIIGISLGCTLLVLVLAVLLVYVYCLKMKTLNRSASSAETADKLLSGVSGYVSKPT 304
 Sbjct 241 IRLPVIIGISLGCTLLVLVLAVLLVYVYCLKMKTLNRSASSAETADKLLSGVSGYVSKPT 300

Query 305 MYETDAIMEATMNLSEQCKIGESVYKA 331
 Sbjct 301 MYETDAIMEATMNLSEQCKIGESVYKA 327

>**dbj|BAG85176.1| Nod factor receptor protein [Glycine max]**

Length=327

Score = 670 bits (1728), Expect = 0.0, Method: Compositional matrix adjust.
 Identities = 325/327 (99%), Positives = 326/327 (99%), Gaps = 0/327 (0%)

Query 5 FPFPLHHSQILC1V1MLFSTNIVQAQSQQDNRTNFSCPSDSDPPSCETYVTVIAQSPNFLSL 64
 Sbjct 1 FPFPLHHSQILC1V1MLFSTNIVQAQSQQDNRTNFSCPSDSDPPSCETYVTVIAQSPNFLSL 60

Query 65 TNISNIFDTSPSLSIARASNLLEPMDDKLVQDQVLLVPVTCGCTGNRSFANISYEINQGDSF 124
 Sbjct 61 TNISNIFDTSPSLSIARASNLLEPMDDKLVQDQVLLVPVTCGCTGNRSFANISYEINQGDSF 120

Query 125 YFVATTSYENLTNWRAVMDLNPVLSPNPKLPIGIQVVFPLFCCKCPSKNQLDKEIKYLITYV 184
 Sbjct 121 YFVATTSYENLTNWRAVMDLNPVLSPNPKLPIGIQVVFPLFCCKCPSKNQLDKEIKYLITYV 180

Query 185 WKGDNVSLVSDKFGASPEDIMSENNYQONFTAANNLPVLIPVTRLPVLARSPSDGRKGG 244
 Sbjct 181 WKGDNVSLVSDKFGASPEDIMSENNYQONFTAANNLPVLIPVTRLPVLARSPSDGRKGG 240

Query 245 IRLPVIIGISLGCTLLVLVLAVLLVYVYCLKMKTLNRSASSAETADKLLSGVSGYVSKPT 304
 Sbjct 241 IRLPVIIGISLGCTLLVLVLAVLLVYVYCLKMKTLNRSASSAETADKLLSGVSGYVSKPT 300

Query 305 MYETDAIMEATMNLSEQCKIGESVYKA 331
 Sbjct 301 MYETDAIMEATMNLSEQCKIGESVYKA 327

>**dbj|BAG85153.1| Nod factor receptor protein [Glycine soja]**

Length=327

Score = 669 bits (1727), Expect = 0.0, Method: Compositional matrix adjust.
 Identities = 325/327 (99%), Positives = 325/327 (99%), Gaps = 0/327 (0%)

Query 5 FPFPLHHSQILC1V1MLFSTNIVQAQSQQDNRTNFSCPSDSDPPSCETYVTVIAQSPNFLSL 64
 Sbjct 1 FPFPLHHSQILC1V1MLFSTNIVQAQSQQDNRTNFSCPSDSDPPSCETYVTVIAQSPNFLSL 60

Query 65 TNISNIFDTSPSLSIARASNLLEPMDDKLVQDQVLLVPVTCGCTGNRSFANISYEINQGDSF 124
 Sbjct 61 TNISNIFDTSPSLSIARASNLLEPMDDKLVQDQVLLVPVTCGCTGNRSFANISYEINQGDSF 120

Query 125 YFVATTSYENLTNWRAVMDLNPVLSPNPKLPIGIQVVFPLFCCKCPSKNQLDKEIKYLITYV 184
 Sbjct 121 YFVATTSYENLTNWRAVMDLNPVLSPNPKLPIGIQVVFPLFCCKCPSKNQLDKEIKYLITYV 180

Query 185 WKGDNVSLVSDKFGASPEDIMSENNYQONFTAANNLPVLIPVTRLPVLARSPSDGRKGG 244
 Sbjct 181 WKGDNVSLVSDKFGASPEDIMSENNYQONFTAANNLPVLIPVTRLPVLARSPSDGRKGG 240

Query 245 IRLPVIIGISLGCTLLVLVLAVLLVYVYCLKMKTLNRSASSAETADKLLSGVSGYVSKPT 304
 Sbjct 241 IRLPVIIGISLGCTLLVLVLAVLLVYVYCLKMKTLNRSASSAETADKLLSGVSGYVSKPT 300

Query 305 MYETDAIMEATMNLSEQCKIGESVYKA 331
 Sbjct 301 MYETDAIMEATMNLSEQCKIGESVYKA 327

>**dbj|BAG85155.1| Nod factor receptor protein [Glycine soja]**

Length=327

Score = 669 bits (1726), Expect = 0.0, Method: Compositional matrix adjust.
 Identities = 325/327 (99%), Positives = 325/327 (99%), Gaps = 0/327 (0%)

Query 5 FPFPLHHSQILC1V1MLFSTNIVQAQSQQDNRTNFSCPSDSDPPSCETYVTVIAQSPNFLSL 64
 Sbjct 1 FPFPLHHSQILC1V1MLFSTNIVQAQSQQDNRTNFSCPSDSDPPSCETYVTVIAQSPNFLSL 60

Query 65 TNISNIFDTSPSLSIARASNLLEPMDDKLVQDQVLLVPVTCGCTGNRSFANISYEINQGDSF 124
 Sbjct 61 TNISNIFDTSPSLSIARASNLLEPMDDKLVQDQVLLVPVTCGCTGNRSFANISYEINQGDSF 120

Query 125 YFVATTSYENLTNWRAVMDLNPVLSPNPKLPIGIQVVFPLFCCKCP SKNQLDKEIKYLITYV 184
 Sbjct 121 YFVATTSYENLTNWRAVMDLNPVLSPNPKLPIGIQVVFPLFCCKCP SKNQLDKEIKYLITYV 180

Query 185 WKGDNVSLVSDKFGASPEDIMSENNYQONFTAANNLPVLIPVTRLPVLARSPSDGRKGG 244
 Sbjct 181 WKGDNVSLVSDKFGASPEDIMSENNYQONFTAANNLPVLIPVTRLPVLARSPSDGRKGG 240

Query 245 IRLPVIIGISLGCTLLVLVLAVLLVYVYCLKMKTLNRSASSAETADKLLSGVSGYVSKPT 304
 Sbjct 241 IRLPVIIGISLGCTLLVLVLAVLLVYVYCLKMKTLNRSASSAETADKLLSGVSGYVSKPT 304

Subjct 241 IRLPVIIGISLGCTLLVLVLAFLVVYVYCLKMKTLNRSASSAETADKLLSGVSGYVSKPT 300

Query 305 MYETDAIMEATMNLSEQCKIGESVYKA 331

Subjct 301 MYETDAIMEATMNLSEQCKIGESVYKA 327

>**dbj|BAG85163.1| Nod factor receptor protein [Glycine max]**
Length=327

Score = 669 bits (1726), Expect = 0.0, Method: Compositional matrix adjust.
Identities = 325/327 (99%), Positives = 325/327 (99%), Gaps = 0/327 (0%)

Query 5 FPFPLPLHSQILC1LVIIMLFSTNIVAQSQQDNRTNFSCPSDSSPPSCETYVTVIAQSPNFLSL 64
FPFPLPLHSQILC1LVIIMLFSTNIVAQSQQDNRTNFSCPSDSSPPSCETYVTVIAQSPNFLSL 60

Subjct 1 FPFPLPLHSQILC1LVIIMLFSTNIVAQSQQDNRTNFSCPSDSSPPSCETYVTVIAQSPNFLSL 60
TNISNIFDTSPS1IARASNLLEPMDDKLVQDQVLLVPVTCGCTGNRSFANISYEINQGDSF 124
TNISNIFDTSPS1IARASNLLEPMDDKLVQDQVLLVPVTCGCTGNRSFANISYEINQGDSF 120

Query 65 TNISNIFDTSPS1IARASNLLEPMDDKLVQDQVLLVPVTCGCTGNRSFANISYEINQGDSF 124
TNISNIFDTSPS1IARASNLLEPMDDKLVQDQVLLVPVTCGCTGNRSFANISYEINQGDSF 120

Subjct 61 TNISNIFDTSPS1IARASNLLEPMDDKLVQDQVLLVPVTCGCTGNRSFANISYEINQGDSF 120
YFVATTTSYENLTNWRAVMMDLNPVLPSPNKLPIGIQVVFPFLFCPKCPSKNQLDKEIKYLITYV 184
YFVATTTSYENLTNWRAVMMDLNPVLPSPNKLPIGIQVVFPFLFCPKCPSKNQLDKEIKYLITYV 180

Query 125 YFVATTTSYENLTNWRAVMMDLNPVLPSPNKLPIGIQVVFPFLFCPKCPSKNQLDKEIKYLITYV 184
Subjct 121 YFVATTTSYENLTNWRAVMMDLNPVLPSPNKLPIGIQVVFPFLFCPKCPSKNQLDKEIKYLITYV 180

Query 185 WKPGDNVSLVSDKGASPEDIMSENNYQGNFTAANNLPLVLPVTRPLPVLRSPSDGRKGG 244
WKPGDNVSLVSDKGASPEDIMSENNYQGNFTAANNLPLVLPVTRPLPVLRSPSDGRKGG 240

Subjct 181 WKPGDNVSLVSDKGASPEDIMSENNYQGNFTAANNLPLVLPVTRPLPVLRSPSDGRKGG 240
IRLPVIIGISLGCTLLVLVLAFLVVYVYCLKMKTLNRSASSAETADKLLSGVSGYVSKPT 304

Query 245 IRLPVIIGISLGCTLLVLVLAFLVVYVYCLKMKTLNRSASSAETADKLLSGVSGYVSKPT 304

Subjct 241 IRLPVIIGISLGCTLLVLVLAFLVVYVYCLKMKTLNRSASSAETADKLLSGVSGYVSKPT 300

Query 305 MYETDAIMEATMNLSEQCKIGESVYKA 331

Subjct 301 MYETDAIMEATMNLSEQCKIGESVYKA 327

>**dbj|BAG85173.1| Nod factor receptor protein [Glycine max]**
Length=327

Score = 669 bits (1725), Expect = 0.0, Method: Compositional matrix adjust.
Identities = 325/327 (99%), Positives = 325/327 (99%), Gaps = 0/327 (0%)

Query 5 FPFPLPLHSQILC1LVIIMLFSTNIVAQSQQDNRTNFSCPSDSSPPSCETYVTVIAQSPNFLSL 64
FPFPLPLHSQILC1LVIIMLFSTNIVAQSQQDNRTNFSCPSDSSPPSCETYVTVIAQSPNFLSL 60

Subjct 1 FPFPLPLHSQILC1LVIIMLFSTNIVAQSQQDNRTNFSCPSDSSPPSCETYVTVIAQSPNFLSL 60
TNISNIFDTSPS1IARASNLLEPMDDKLVQDQVLLVPVTCGCTGNRSFANISYEINQGDSF 124
TNISNIFDTSPS1IARASNLLEPMDDKLVQDQVLLVPVTCGCTGNRSFANISYEINQGDSF 120

Query 65 TNISNIFDTSPS1IARASNLLEPMDDKLVQDQVLLVPVTCGCTGNRSFANISYEINQGDSF 124
TNISNIFDTSPS1IARASNLLEPMDDKLVQDQVLLVPVTCGCTGNRSFANISYEINQGDSF 120

Subjct 61 TNISNIFDTSPS1IARASNLLEPMDDKLVQDQVLLVPVTCGCTGNRSFANISYEINQGDSF 120
YFVATTTSYENLTNWRAVMMDLNPVLPSPNKLPIGIQVVFPFLFCPKCPSKNQLDKEIKYLITYV 184
YFVATTTSYENLTNWRAVMMDLNPVLPSPNKLPIGIQVVFPFLFCPKCPSKNQLDKEIKYLITYV 180

Query 125 YFVATTTSYENLTNWRAVMMDLNPVLPSPNKLPIGIQVVFPFLFCPKCPSKNQLDKEIKYLITYV 184
Subjct 121 YFVATTTSYENLTNWRAVMMDLNPVLPSPNKLPIGIQVVFPFLFCPKCPSKNQLDKEIKYLITYV 180

Query 185 WKPGDNVSLVSDKGASPEDIMSENNYQGNFTAANNLPLVLPVTRPLPVLRSPSDGRKGG 244
WKPGDNVSLVSDKGASPEDIMSENNYQGNFTAANNLPLVLPVTRPLPVLRSPSDGRKGG 240

Subjct 181 WKPGDNVSLVSDKGASPEDIMSENNYQGNFTAANNLPLVLPVTRPLPVLRSPSDGRKGG 240
IRLPVIIGISLGCTLLVLVLAFLVVYVYCLKMKTLNRSASSAETADKLLSGVSGYVSKPT 304

Query 245 IRLPVIIGISLGCTLLVLVLAFLVVYVYCLKMKTLNRSASSAETADKLLSGVSGYVSKPT 304

Subjct 241 IRLPVIIGISLGCTLLVLVLAFLVVYVYCLKMKTLNRSASSAETADKLLSGVSGYVSKPT 300

Query 305 MYETDAIMEATMNLSEQCKIGESVYKA 331

Subjct 301 MYGTDAIMEATMNLSEQCKIGESVYKA 327

>**dbj|BAG85154.1| Nod factor receptor protein [Glycine soja]**
Length=327

Score = 667 bits (1720), Expect = 0.0, Method: Compositional matrix adjust.
Identities = 324/327 (99%), Positives = 325/327 (99%), Gaps = 0/327 (0%)

Query 5 FPFPLPLHSQILC1LVIIMLFSTNIVAQSQQDNRTNFSCPSDSSPPSCETYVTVIAQSPNFLSL 64
FPFPLPLHSQILC1LVIIMLFSTNIVAQSQQDNRTNFSCPSDSSPPSCETYVTVIAQSPNFLSL 60

Subjct 1 FPFPLPLHSQILC1LVIIMLFSTNIVAQSQQDNRTNFSCPSDSSPPSCETYVTVIAQSPNFLSL 60
TNISNIFDTSPS1IARASNLLEPMDDKLVQDQVLLVPVTCGCTGNRSFANISYEINQGDSF 124
TNISNIFDTSPS1IARASNLLEPMDDKLVQDQVLLVPVTCGCTGNRSFANISYEINQGDSF 120

Query 65 TNISNIFDTSPS1IARASNLLEPMDDKLVQDQVLLVPVTCGCTGNRSFANISYEINQGDSF 124
TNISNIFDTSPS1IARASNLLEPMDDKLVQDQVLLVPVTCGCTGNRSFANISYEINQGDSF 120

Subjct 61 TNISNIFDTSPS1IARASNLLEPMDDKLVQDQVLLVPVTCGCTGNRSFANISYEINQGDSF 120
YFVATTTSYENLTNWRAVMMDLNPVLPSPNKLPIGIQVVFPFLFCPKCP SKNQLDKEIKYLITYV 184
YFVATTTSYENLTNWRAVMMDLNPVLPSPNKLPIGIQVVFPFLFCPKCP SKNQLDKEIKYLITYV 180

Query 125 YFVATTTSYENLTNWRAVMMDLNPVLPSPNKLPIGIQVVFPFLFCPKCP SKNQLDKEIKYLITYV 184
Subjct 121 YFVATTTSYENLTNWRAVMMDLNPVLPSPNKLPIGIQVVFPFLFCPKCP SKNQLDKEIKYLITYV 180

Query 185 WKPGDNVSLVSDKGASPEDIMSENNYQGNFTAANNLPLVLPVTRPLPVLRSPSDGRKGG 244
WKPGD+VSLVSDKGASPEDIMSENNY QNFTAANNLPLVLPVTRPLPVLRSPSDGRKGG 240

Subjct 181 WKPGDDVSLVSDKGASPEDIMSENNYDQNFTAANNLPLVLPVTRPLPVLRSPSDGRKGG 240
IRLPVIIGISLGCTLLVLVLAFLVVYVYCLKMKTLNRSASSAETADKLLSGVSGYVSKPT 304

Query 245 IRLPVIIGISLGCTLLVLVLAFLVVYVYCLKMKTLNRSASSAETADKLLSGVSGYVSKPT 304

Subjct 241 IRLPVIIGISLGCTLLVLVLAFLVVYVYCLKMKTLNRSASSAETADKLLSGVSGYVSKPT 300

Query 305 MYETDAIMEATMNLSEQCKIGESVYKA 331

Subjct 301 MYETDAIMEATMNLSEQCKIGESVYKA 327

>**dbj|BAG85169.1| Nod factor receptor protein [Glycine max]**
Length=327

Score = 665 bits (1717), Expect = 0.0, Method: Compositional matrix adjust.
Identities = 324/327 (99%), Positives = 325/327 (99%), Gaps = 0/327 (0%)

Query 5 FPFPLPLHSQILC1LVIIMLFSTNIVAQSQQDNRTNFSCPSDSSPPSCETYVTVIAQSPNFLSL 64
FPFPLPLHSQILC1LVIIMLFSTNIVAQSQQDNRTNFSCPSDSSPPSCETYVTVIAQSPNFLSL

Query 65 TNISNIFDTSPLSIARASNLPEPMDDKLVQDQVLLPVTCGCTGNRSFANISYEINQGDSF 124
 TNISNIFDTSPLSIARASNLPEPMDDKLVQDQVLLPVTCGCTGNRSFANISYEINQGDSF
 Sbjct 61 TNISNIFDTSPLSIARASNLPEPMDDKLVQDQVLLPVTCGCTGNRSFANISYEINQGDSF 120
 Query 125 YFWATTTSYENLTNWRAVMDDLNPLVSLSPNKLPIGIQVVVFPLFCCKCPSKNQLDKEIKYLITYV 184
 YFWATTTSYENLTN RAVMDLNPVSLSPNKLPIGIQVVVFPLFC+CPSKNQLDKEIKYLITYV
 Sbjct 121 YFWATTTSYENLTN RAVMDLNPVSLSPNKLPIGIQVVVFPLFCCECPSKNQLDKEIKYLITYV 180
 Query 185 WKGDNVSLVSDKFGASPEDIMSENNYQNFATAANNLPVLIPVTRLPVLARSPSDGRKGG 244
 WKGDNVSLVSDKFGASPEDIMSENNYQNFATAANNLPVLIPVTRLPVLARSPSDGRKGG
 Sbjct 181 WKGDNVSLVSDKFGASPEDIMSENNYQNFATAANNLPVLIPVTRLPVLARSPSDGRKGG 240
 Query 245 IRLPVIIGISLGCTLLVVLAVLILVYVYCLMKMKTLNRSASSAETADKLLSGVSGYVSKPT 304
 IRLPVIIGISLGCTLLVVLAVLILVYVYCLMKMKTLNRSASSAETADKLLSGVSGYVSKPT
 Sbjct 241 IRLPVIIGISLGCTLLVVLAVLILVYVYCLMKMKTLNRSASSAETADKLLSGVSGYVSKPT 300
 Query 305 MYETDAIMEATMNLSEQCKIGESVYKA 331
 MYETDAIMEATMNLSEQCKIGESVYKA
 Sbjct 301 MYETDAIMEATMNLSEQCKIGESVYKA 327

>**dbj|BAG85166.1| Nod factor receptor protein [Glycine max]**

Length=327

Score = 660 bits (1702), Expect = 0.0, Method: Compositional matrix adjust.
 Identities = 320/324 (98%), Positives = 322/324 (99%), Gaps = 0/324 (0%)

Query 5 FPFPLHSQILC1VIMLFSTNIVAQSQQDNRTNFSCPSDSSPCSETYVTYIAQSPNFLSL 64
 FPFPLHSQILC1VIMLFSTNIVAQSQQDNRTNFSCPSDSSPCSETYVTYIAQSPNFLSL
 Sbjct 1 FPFPLHSQILC1VIMLFSTNIVAQSQQDNRTNFSCPSDSSPCSETYVTYIAQSPNFLSL 60
 Query 65 TNISNIFDTSPLSIARASNLPEPMDDKLVQDQVLLPVTCGCTGNRSFANISYEINQGDSF 124
 TNISNIFDTSPLSIARASNLPEPMDDKLVQDQVLLPVTCGCTGNRSFANISYEINQGDSF
 Sbjct 61 TNISNIFDTSPLSIARASNLPEPMDDKLVQDQVLLPVTCGCTGNRSFANISYEINQGDSF 120
 Query 125 YFWATTTSYENLTNWRAVMDDLNPLVSLSPNKLPIGIQVVVFPLFCCKCPSKNQLDKEIKYLITYV 184
 YFWATTTSYENLTN RAVMDLNPVSLSPNKLPIGIQVVVFPLFCCKCPSKNQLDKEIKYLITYV
 Sbjct 121 YFWATTTSYENLTN RAVMDLNPVSLSPNKLPIGIQVVVFPLFCCKCPSKNQLDKEIKYLITYV 180
 Query 185 WKGDNVSLVSDKFGASPEDIMSENNYQNFATAANNLPVLIPVTRLPVLARSPSDGRKGG 244
 WKGDNVSLVSDKFGASPEDIMSENNYQNFATAANNLPVLIPVTRLPVLARSPSDGRKGG
 Sbjct 181 WKGDNVSLVSDKFGASPEDIMSENNYQNFATAANNLPVLIPVTRLPVLARSPSDGRKGG 240
 Query 245 IRLPVIIGISLGCTLLVVLAVLILVYVYCLMKMKTLNRSASSAETADKLLSGVSGYVSKPT 304
 IRLPVIIGISLGCTLLVVLAVLILVYVYCLMKMKTLNRSASSAEE ADKLLSGVSGYVSKPT
 Sbjct 241 IRLPVIIGISLGCTLLVVLAVLILVYVYCLMKMKTLNRSASSAENADKLLSGVSGYVSKPT 300
 Query 305 MYETDAIMEATMNLSEQCKIGESV 328
 MYETDAIMEATMNLSEQCKIGESV
 Sbjct 301 MYETDAIMEATMNLSEQCKIGESV 324

>**dbj|BAG85147.1| Nod factor receptor protein [Glycine soja]**

Length=327

Score = 659 bits (1700), Expect = 0.0, Method: Compositional matrix adjust.
 Identities = 320/327 (97%), Positives = 321/327 (98%), Gaps = 0/327 (0%)

Query 5 FPFPLHSQILC1VIMLFSTNIVAQSQQDNRTNFSCPSDSSPCSETYVTYIAQSPNFLSL 64
 FPFPLHSQILC1VIMLFSTNIVAQSQQDNRTNFSCPSDSSPCSETYVTYIAQSPNFLSL
 Sbjct 1 FPFPLHSQILC1VIMLFSTNIVAQSQQDNRTNFSCPSDSSPCSETYVTYIAQSPNFLSL 60
 Query 65 TNISNIFDTSPLSIARASNLPEPMDDKLVQDQVLLPVTCGCTGNRSFANISYEINQGDSF 124
 TNISNIFDTSPLSIARASNLPEPMDDKLVQDQVLLPVTCGCTGNRSFANISYEINQGDSF
 Sbjct 61 TNISNIFDTSPLSIARASNLPEPMDDKLVQDQVLLPVTCGCTGNRSFANTSYEINQGDSF 120
 Query 125 YFWATTTSYENLTNWRAVMDDLNPLVSLSPNKLPIGIQVVVFPLFCCKCPSKNQLDKEIKYLITYV 184
 YFWATTTSYENLTN RAVMDLNPVSLSPNKLPIGIQVVVFPLFCCKCPSKNQLDKEIKYLITYV
 Sbjct 121 YFWATTTSYENLTN RAVMDLNPVSLSPNKLPIGIQVVVFPLFCCKCPSKNQLDKEIKYLITYV 180
 Query 185 WKGDNVSLVSDKFGASPEDIMSENNYQNFATAANNLPVLIPVTRLPVLARSPSDGRKGG 244
 WKGDNVSLVSDKFGASPEDIMSENNYQNFATAANNLPVLIPVTRLPVLARSPSDGRKGG
 Sbjct 181 WKGDNVSLVSDKFGASPEDIMSENNYQNFATAANNLPVLIPVTRLPVLARSPSDGRKGG 240
 Query 245 IRLPVIIGISLGCTLLVVLAVLILVYVYCLMKMKTLNRSASSAETADKLLSGVSGYVSKPT 304
 IRLPVIIGIT+LGCTLLVVLAY CLMKMKTLNRSASSAETADKLLSGVSGYVSKPT
 Sbjct 241 IRLPVIIGIT+LGCTLLVVLASWYGYCLMKMKTLNRSASSAETADKLLSGVSGYVSKPT 300
 Query 305 MYETDAIMEATMNLSEQCKIGESVYKA 331
 MYETDAIMEATMNLSEQCKIGESVYKA
 Sbjct 301 MYETDAIMEATMNLSEQCKIGESVYKA 327

>**ref|XP_002269472.1| PREDICTED: hypothetical protein [Vitis vinifera]**

emb|CBI17584.3| unnamed protein product [Vitis vinifera]
 Length=590

GENE ID: 100259809 LOC100259809 | hypothetical protein LOC100259809
 [Vitis vinifera] (10 or fewer PubMed links)

Score = 654 bits (1688), Expect = 0.0, Method: Compositional matrix adjust.
 Identities = 341/579 (58%), Positives = 424/579 (73%), Gaps = 7/579 (1%)

Query 23 STN-IVAQSQQDNRTNFSCPSDSSPCSETYVTYIAQSPNFLSLTNISNIFDTSPLSIARA 81
 STN I AQS TNFSC +DSP SC+TYV Y AQ+P FL + NIS+F S LSIA A
 Sbjct 16 STNHITAQSPATPPVNTNFSCCTTDSASCQTYVYIYRAQAPGFLDVGNIISDLFGISRLSIAEA 75
 Query 82 SNLEPMDDDKLVQDQVLLPVTCGCTGNRSFANISYEINQGDSFYFVATTTSYENLTNWRAV 141
 SNL + L DQ+LLVP+ C CTGN FAN+Y+I DSTYFV+ T +ENLTN+ AV
 Sbjct 76 SNLASEEARLSPDQLLLVPILCSCCTGNHYFANITYKIKTDDSFYFVSFTVFEMLTNYNNAV 135
 Query 142 MDLNPVLSPKLPIGIQVVVFPLFCCKCP SKNQLDKEIKYLITYVWKPGDNVSLVSDKFGAS 201
 INP L P L +G++VVFPFLFCCKCP SK+ DK I YLITYVW+PGD+V LV AS
 Sbjct 136 EALNPGLEPTTLQVGVEVVFPLFCCKCP SKSHSDKGINYLITYVWQPGDDVLLVGTNLKAS 195

Query	202	PEDIMSENNYQGNFTAANNLPLVILPVTRLPVLARSPSDGRKGIRLPVIIGISLGCTLLV P DI ENN NF+A+ P VLIIPV++ P+L + KG R + + +S G L+	261
Sbjct	196	PVDIREDENN-NLNFSASVDQPVLIIPVSQPPPLTQPERRASKG--RWILALVLTGALLIF	252
Query	262	LVLAVLVLVYVYCLMKMTLNRASSAETAD--KLLSGVSGYVSKPTMYETDAIMEATMNL L+++L+ K KTL+ S SS ET D KLL GVSGY+ KP MYET IMEATMNL+	319
Sbjct	253	LLVSLLVYTGLIRKKTLDHSESSLETTDLIKLLPGVSGYLGKPIMYETKVIMEATMNLN	312
Query	320	EQCKIGESVYKANIEGKVLAVKRFKEDVTEELKILQKVNHGNLVKLMGVSSDMDGNCFVV E +IG SVY+A I G+V+AVK+ KED+TEEL+ILQKVNHGNLVKLMGVSSD DGN F+V	379
Sbjct	313	EHYRIGGSVYRATINGQVVAVKKTKEDEITEELRLQKVNHGNLVKLMGVSSDADGNRFLV	372
Query	380	YEYAENGSLDEWLFSKSCSDTSNSRASLTWCQRISMAVDVAMGLQYMHEAYPRIVHRDI YE+AENGSLD+WL K S +S+ A LTW QRI +A+DVA GLQYMHEH P +VHRDI	439
Sbjct	373	YEFAENGSLDKWLHPKPSSPSSSV-AFLTWSQRIVQLVALDVANGLQYMHEHTQPSVVRDI	431
Query	440	TSSNILLDSNFKA KIANFSMARTFTNPMPKIDVFAFGVVLIELLTGRKAMTTKENGEVV ++NILLDS FKAKIANFSMA N MMKP+DVAFGVVL+ELL+G+KAM +NGE+V	499
Sbjct	432	RANNILLDSRSFKAKIANFSMATTAMNSMMPKVDVFAFGVVLIELLSGKAMQM RANGEIV	491
Query	500	MLWKDIWKLQDFQEENREERLKKWMDPKLESYYPIDYALSLASLAVNCTADKSLSRPTIAE MLWKDI +I + E+ RE+R++WMDP LE++YP D AL+LA LA +CT +KS +RP+AE	559
Sbjct	492	MLWKDIREILEVEDKREDRIRRWMDPTLENFYPFDGALNLAGLARSCTQEKSARPSMAE	551
Query	560	IVLSSLSSLTQPSPATLERSLTSSGLDVEATQIVTSIAAR 598 I +LS+L+Q S TLERS T E QI+ + AR	
Sbjct	552	IAFNLSVLSQTSETLERSWTQGFPEETIQIINPVIAR 590	

>ref|XP_002533280.1| serine-threonine protein kinase, plant-type, putative [Ricinus communis]
 >b|EEF29112.1| serine-threonine protein kinase, plant-type, putative [Ricinus communis]
 Length=620

GENE ID: 8272992 RCOM_0411680 | serine-threonine protein kinase, plant-type, putative [Ricinus communis]

Score = 638 bits (1645), Expect = 0.0, Method: Compositional matrix adjust.
 Identities = 337/603 (55%), Positives = 427/603 (70%), Gaps = 32/603 (5%)

Query	23	STNIVAQSQQDNRTNFSCPSDSPSCETYVTYIAQSPNFLSLTNISNIFDTSPLSIARAS +T + AQS Q TNFSC D P C+TYV Y AQ PNFL+L NIS+F S LSIA AS	82
Sbjct	23	TTYVTAQSPQG--TNFSCSVLDLSPCQTYVAYYAQPPNFLNLGNISDLFAVRSRLSIASAS	80
Query	83	NLEPMDDKLVQDQVLLPVTCGCTGNRSFANISYEINQGDSFYFVATTSYENLTNWRAVM NL D L+ +Q+L+T+TCGCTGN SFANI+Y+I GDSFYF+T+ +ENL W+AV	142
Sbjct	81	NLVSEDIPLMNPQLLVPITCGCTGNSSFANITYQIKPGDSFYFVSTTYFENLAKWQAVE	140
Query	143	DLPNVLPSPNKLPIQVVFPLFCPKPSKNQLDEIKYLITYVWKGPDNVSLVSDKFGASP NP L P L G +VVFPLFCPKPSKNQ+ I+YLITYVW+P D++ V KF ASP	202
Sbjct	141	SFPNPNLDPFTLLHPGDKVVFPLFCPKPSKNQMKRGIQYLITYVWQPEDDIFKVGAKFNASP	200
Query	203	EDIMSENNYQGNFTAANNLPLVILPVTRLPVLAR-SPSDGRKGIRLPVIIGISLGCTLLV DI +NNY +F+ A + P+LIPV++P+L++ SPS ++ L +II S+ LL+	261
Sbjct	201	HDIAIQNYYW-DFSTAVHHPLLPTQMPILSQPSPSWPQRSEHHLVIIIVTSVAGALLI	259
Query	262	LVLAVLVLVYVYC----LKMKTILNRASSAETA-----DKLLSGV +L LV+ +C K TI+R+ S ET DKLL GV	296
Sbjct	260	FLLVAFLVHAHCSCKKKKTMLHRNGSCLETDQLIKEQGKYRSFEKIIQDKLLPGV	319
Query	297	SGYVSKPTMYETDAIMEATMNLSSEQCKIGESVYKANIEGKVLAVKRFKEDVTEELKILQK SGY+ KP MY+ I+ ATM+L E +IG SVY+ANI G+VIAV+ K D+TEEL ILQK	356
Sbjct	320	SGYLGKPIMYDIKEILLATMDLHEHYRIGGSVYRANINGQVIAVKKTKVDITEELNQK	379
Query	357	VNHGNLVKLMGVSSDNDGNCFVVEYAYAENGSLDEWLFSKSCSDTSNSRASLTWCQRISMA VNH NLVKLMLG+SS+ DG+CF+VVEYAENGSLD+WL K + +S+S A L+W QR+ +A	416
Sbjct	380	VNHANLVKLMGISSNADGDCFLVYAYAENGSLDKWLHPKP-ASSSSVAFLSWSQRLQIA	438
Query	417	VDVAMGLQYMHEAYPRIVHRDITSSNILLDSNFKA KIANFSMARTFTNPMPKIDVFAF +DVA GLQYMHEH P +VH DI +SNILLDS FKAKIANFS+A+ T4 M+ K+DVFAF	476
Sbjct	439	LDVASGLQYMHEHIQPTVHMDIIRTSNILLDSRFKA KIANFSVAKLTDMSLQKVDFAF	498
Query	477	GVVLLIELTGRKAMTTKENGEVVMLWKKDIWKFIDQEEENREERLKKWMDPKLESYYPIDYA GVV1+ELL G+KAM T ENGE+V+LWK++ + + E R ERLIK MDP LE++YPID A	536
Sbjct	499	GVVLLLELLCGKKAMVTNENGEIVLLWKEMGVMEVAEKRAERLKKRMDPNLENFYPIDSA	558
Query	537	LSLASLAVNCTADKSLSRPTIAEIVLSSLTQPSPATLERSLTSSGLDVEA-TQIVTSI LSLA+LA CT +KS +RP++AEIV +L++LTQ TLERS T SGL+ E QI + +	595
Sbjct	559	LSLANLARVCTLEKSSARPSMAEIVFNLTVLTQSCSETLERSWT-SGLEAEEDIQITSPV	617
Query	596	AAR 598 AR	
Sbjct	618	IAR 620	

>ref|XP_002310198.1| predicted protein [Populus trichocarpa]

>b|EEE90648.1| predicted protein [Populus trichocarpa]
 Length=601

GENE ID: 7473142 POPTRDRAFT_870366 | hypothetical protein [Populus trichocarpa]
 (10 or fewer PubMed links)

Score = 614 bits (1583), Expect = 1e-173, Method: Compositional matrix adjust.
 Identities = 328/595 (55%), Positives = 423/595 (71%), Gaps = 17/595 (2%)

Query	14	IICLIVMLFSTNIVAQSQQDNRTNFSCPSDSPSCETVVTYIAQSPNFLSLTNISNIFDT + LV++ FST + AQt TNFSCP DSP SC TY++Y+AQ P+FL L IS++F	73
Sbjct	14	LFVLVLFVFFSTYVTAQAPPG--TNFSCPVDSPTSCPTYISYLAQPPDFLDLGKISHLFGI	71
Query	74	SPLSIARASNLEPMDDKLVLKDQVLLPVTCGCTGNRSFANISYEINQGDSFYFVATTSYE S IA ASN L D L +Q+LWP+ CGCTG++SF NI++I QGDS Y V+T S+E	133
Sbjct	72	SRTLTIASASNLVSEDTPLFPNQLLVPIRCGCTGSQSFVNITYQIQQGDSIYSVSTISFE	131
Query	134	NLTNWRAVMDLNPNVLPSPNKLPIGIVQVFPLFCKCPSKNQLDKEIKYLITYVWKGDNVSL NLT W+ V LN L+P L G +V+FPLFCKCP+ L+ I++LITYVW+PGD++	193

Subjct 132 NLTRWQEVEALNRSITPTLLHAGDEVIFPLFCKCPSRTHLENGIEHLITYVWQPGDDLKK 191
 Query 194 VSDKFGASPEDIMSENNYGQNFTAANNILPVLIPVTRLPVALAR---SPSDGRKGIGIRL-PV 249
 V+ AS +I ENNY NF AA P+IPV++LPVL++ +P R+G L V
 Subjct 192 VAAMLNASERNIVENNY-DNFNAAVYNPIVIPVSKLPLVLSQPYLTPE--RRGSKHLWIV 248
 Query 250 IIGISLGCTLLVLVLAFLVLYVY--LKMKTLNRSASSAETAD--KLLSGVSGYVSKPTM 305
 I+ S+ T L L++ C K L+R+ S ET+D KLL GV G + K +
 Subjct 249 IVAASIASTFFTCPLVAFLIHKRCSYKATKALDRTGSLETSPPDKLIPGVLCCLDKSII 308
 Query 306 YETDAIMEATMNLSEQCKIGESVYKANIEGKVLAVKRFKEDVTEELKILQKVNHGNLVKL 365
 YE AIME TM+L E KIC SVY+ANI G VLAVK+ K+DVTEELKILQKV+H NLVKL
 Subjct 309 YEVKAIMECTMDLHEHYKIGGSVYRANINGCVIAVKKTKDDVTEELKILQKVSHANLVKL 368
 Query 366 MGVSDDND--GNCFVYYEYAENGSLDEWLFSKSCSDTSNSRASLTWCQRISMADVAMGL 423
 MG+SS++D GN F+VYEYAENGSLD+WL KS +S+S LTW QR+ +A+DVA GL
 Subjct 369 MGMSSESDREGNRFLVYEAENGSLDKWLHPKS-ESSSSVGFLTWKQRMQVALDVANGL 427
 Query 424 QYMEHAYPRIVHRDITSSNILLDSNFKAKIANFSMARTFTNPMMPKIDVFAFGVLLIEL 483
 QY+HEH PR VH+DI +SNILLS F+AKIANFSMAR T+ MMPK DVF FGVVL+EL
 Subjct 428 QYLHEHTQPRTRVHKDIRTSNILLSTFRAKIANFSMARAATDSSMPKDDVFDGFVVLLEL 487
 Query 484 LTGRKAMTTKENGEVVMLWKDIWKFQDEENREERLKKWMDPKLESYYPIDYASLASLA 543
 L+G+KAM TKE GE+V+L ++I + + EE REERL+KWMMP LE +YPID A+SLA+LA
 Subjct 488 LSGKAMMTKEGEIVLICREIKDVLEMEEKREERLKKWMDPNLERFYPIIDSAMSLATLA 547
 Query 544 VNCTADKSLSRPTIAEIVLSSLTQPSPATLERSLTSSGLDVEATQIVTSIAAR 598
 CT +KS RP++AEIV +L++LTQ SP TLER TS +T++V+ + AR
 Subjct 548 RLCTLEKSSERPSMAEIVFNLTQSSPETLER-WTSEVETEDFTRLVSPVTAR 601

>emb|CA002936.1| LysM-domain containing receptor-like kinase [Medicago truncatula]
 var. truncatula]
 Length=349

Score = 499 bits (1285), Expect = 4e-139, Method: Compositional matrix adjust.
 Identities = 248/351 (70%), Positives = 290/351 (82%), Gaps = 4/351 (1%)

Query 54 YIAQSPNFLSLTNISNIFDTSPSLSIARASNLEPMDDKLVVKDQVLLPVTCGCTGNRSFAN 113
 Y AQSPNFLSL+NIS+IF+ SPL IA+ASN+E D KL+ DQ+LLPVTCGCT N SFAN
 Subjct 1 YRAQSPNFLSLNSNISDIFNLSPLRRIAKASNIEAEDKKLIPDQLLLVPVTCGCTKNHSFAN 60
 Query 114 ISYEINQGDSFYFVATTSYENLTNWRAVMMDLNPLSPNKLPIGIQVVFPFLFKCP SKNQL 173
 I+Y I QGD+F+ ++ TSY+NLTN+ + NP LSP LP+ +V PLFCKCP SKNQL
 Subjct 61 ITYSIKQGDNNFILSITSYQNLNTYLEFKNFNPNLSPTLPLDTKVSVPFLFKCP SKNQL 120
 Query 174 DKEIKYLITYVWKPGDNVSLVSDKFGASPEDIMSENNYGQNFTAANNILPVLIPVTRLPV 233
 +K IKYLITYVW+ DNV+LVS KFGAS +--+ENN+ NFTA+ N VLIPVT LP L
 Subjct 121 NGKIKYLITYVQWDNDNVTLVSSSKFGASQVEMLAENNHH--NFTASTNRSVLIPVTSPLKL 178
 Query 234 ARSPSDGRKGIGIRLPVIIGISLGCTLLVLVLAFLVLYVYCLMKTLNRSASSAETADKL 292
 + S+GRK + L +IIGISLG +LVL + LVVYCLMK LNRS SS+ETADKL
 Subjct 179 DQPSSNGRKSSSQNLALIIGISLGSAFFILVLTSLVYVYCLMKRKLNRNSTSSSETADKL 238
 Query 293 LSGVSGYVSKPTMYETDAIMEATMNLSEQCKIGESVYKANIEGKVLAVKRFKEDVTEELK 352
 LSGVSGYVSKPTMYETDAIMEATMNLSEQCKIGESVYKANIEGKVLAVKRFKEDVTEELK
 Subjct 239 LSGVSGYVSKPTMYEIDAIMEGTNLSDNCKIGESVYKANIDGRVLAVKKIKKDASEELK 298
 Query 353 ILQKVNHGNLVKLMLGVSSDNGNCFVYVYEAENGSLDEWLFSKSCSDTSNS 403
 ILQKVNHGNLVKLMLGVSSDNGNCF+VYEYAENGSL+EWLFS+S S TSNS
 Subjct 299 ILQKVNHGNLVKLMLGVSSDNGNCFLVYVYEAENGSLLEEWLFSES-SKTSNS 348

>emb|CA002948.1| LysM-domain containing receptor-like kinase [Medicago truncatula]
 var. truncatula]
 Length=337

Score = 484 bits (1245), Expect = 2e-134, Method: Compositional matrix adjust.
 Identities = 238/339 (70%), Positives = 278/339 (82%), Gaps = 3/339 (0%)

Query 49 ETYVTYIAQSPNFLSLTNISNIFDTSPSLSIARASNLEPMDDKLVVKDQVLLPVTCGCTGN 108
 ETYV Y AQSPNFLSL+NIS+IF+ SPL IA+ASN+E D KL+ DQ+LLPVTCGCT N
 Subjct 1 ETYVAYRAQSPNFLSLNSNISDIFNLSPLRRIAKASNIEAEDKKLIPDQLLLVPVTCGCTKN 60
 Query 109 RSFANISYEINQGDSFYFVATTSYENLTNWRAVMMDLNPLSPNKLPIGIQVVFPFLFKCP 168
 SFANI+Y I QGD+F+ ++ TSY+NLTN+ + NP LSP LP+ +V PLFCKCP
 Subjct 61 HSFANITYSIKQGDNNFILSITSYQNLNTYLEFKNFNPNLSPTLPLDTKVSVPFLFKCP 120
 Query 169 SKNQLDKEIKYLITYVWKPGDNVSLVSDKFGASPEDIMSENNYGQNFTAANNILPVLIPV 228
 SKNQL+K IKYLITYVW+ DNV+LVS KFGAS +--+ENN+ NFTA+ N VLIPVT
 Subjct 121 SKNQLNKGKIKYLITYVQWDNDNVTLVSSSKFGASQVEMLAENNHH--NFTASTNRSVLIPV 178
 Query 229 RLPVLARSISDGRKGIGIRLPVIIGISLGCTLLVLVLAFLVLYVYCLMKTLNRSASSA 287
 LP L + S+GRK + L +IIGISLG +LVL + LVVYCLMK LNRS SS+E
 Subjct 179 SLPKLDQPSNGRKSSSQNLALIIGISLGSAFFILVLTSLVYVYCLMKRKLNRNSTSSSE 238
 Query 288 TADKLLSGVSGYVSKPTMYETDAIMEATMNLSEQCKIGESVYKANIEGKVLAVKRFKEDV 347
 TADKLLSGVSGYVSKPTMYETDAIMEATMNLSEQCKIGESVYKANIEGKVLAVKRFKEDV
 Subjct 239 TADKLLSGVSGYVSKPTMYEIDAIMEGTNLSDNCKIGESVYKANIDGRVLAVKKIKKD 298
 Query 348 TEELKILQKVNHGNLVKLMLGVSSDNGNCFVYVYEAENG 386
 +EELKILQKVNHGNLVKLMLGVSSDNGNCF+VYEYAENG
 Subjct 299 SEELKILQKVNHGNLVKLMLGVSSDNGNCFLVYVYEAENG 337

>emb|CA002942.1| LysM-domain containing receptor-like kinase [Medicago truncatula]
 var. truncatula]
 Length=334

Score = 481 bits (1238), Expect = 1e-133, Method: Compositional matrix adjust.
 Identities = 237/336 (70%), Positives = 277/336 (82%), Gaps = 3/336 (0%)

Query 54 YIAQSPNFLSLTNISNIFDTSPSLSIARASNLEPMDDKLVVKDQVLLPVTCGCTGNRSFAN 113
 Y AQSPNFLSL+NIS+IF+ SPL IA+ASN+E D KL+ DQ+LLPVTCGCT N SFAN
 Subjct 1 YRAQSPNFLSLNSNISDIFNLSPLRRIAKASNIEAEDKKLIPDQLLLVPVTCGCTKNHSFAN 60
 Query 114 ISYEINQGDSFYFVATTSYENLTNWRAVMMDLNPLSPNKLPIGIQVVFPFLFKCP 173
 I+Y I QGD+F+ ++ TSY+NLTN+ + NP LSP LP+ +V PLFCKCP SKNQL

Query 174 DKEIKYLITYVWKPGDNVSLVSDKFGASPEDIMSENNYQGNFTAANNLPVLIPVTRLVPL 233
 +K IKYLYTIVW+ DNV+LVS KFGAS +++ENN+ NFTA+ N VLIPVT LP L
 Sbjct 121 NKGIKYLITYVWQDNDNVTLVSSKFGASQVEMLAENNHH--NFTASTNRSVLIPVTSPLKL 178

Query 234 ARSPSDGRKGGIR-LPVIIGISLGCTLLVLVLA VLLVYVYCLMKTLNRSASSAETADKL 292
 + S+GRK + L +IIGISLG +LVL + LVVYVCLMK LNRS SS+ETADKL
 Sbjct 179 DQPSSNGRKSSSQNIALI IIGISLGS AFFILVITLSLVVYCLMKRNLNRSTSSSETADKL 238

Query 293 LSGVSGYVSKPTMYETDAIMEATMNLSEQCKIGESVYKANIEGKVLA VKRKFEDVTEELK 352
 LSGVSGYVSKPTMYE DAIME TMNLS+ CKIGESVYKANI+G+VLA V+ K+D +EELK
 Sbjct 239 LSGVSGYVSKPTMYEIDAIMEGTINLSDNCKIGESVYKANIDGRVLA VKKIKKDASEELK 298

Query 353 ILQKVNHNGLVKL MGVSSDNDGNCFV VYE AENGSL 388
 ILQKVNHNGLVKL MGVSSDNDGNCF+VYE AENGSL
 Sbjct 299 ILQKVNHNGLVKL MGVSSDNDGNCFLV YEAENGSL 334

>emb|CA002960.1| LysM-domain containing receptor-like kinase [Medicago truncatula]
 var. truncatula]
 Length=333

Score = 477 bits (1228), Expect = 2e-132, Method: Compositional matrix adjust.
 Identities = 235/335 (70%), Positives = 275/335 (82%), Gaps = 3/335 (0%)

Query 54 YIAQSPNFLSLTNISNIFDTSPLSIARASNLEPMDDKLVVDQVLLPVTCGCTGNRSFAN 113
 Y AQSPNFLSL+NIS+IF+ SPL IA+ASN+E D KL+ DQ+LLPVTCGCT N SFAN
 Sbjct 1 YRAQSPNFLSLNSNISDIFNLSPRIAKASNIEADKKLIPDQLLVPVTCGCTKNHSFAN 60

Query 114 ISYEINQGDSFYFVATTSYENLTNWRAVMDLNPLSPNKLPIGIQVVFPLFCCKCP SKNQL 173
 I+Y I QGD+F+ ++ TSY+NLTN+ + NP LSP LP+ +V PLFCCKCP SKNQL
 Sbjct 61 ITYSIKQGDNFFILSITSYQNLNTYLEFKNFNPNLSPTLLPLDKVSVPLFCCKCP SKNQL 120

Query 174 DKEIKYLITYVWKPGDNVSLVSDKFGASPEDIMSENNYQGNFTAANNLPVLIPVTRLVPL 233
 +K IKYLYTIVW+ DNV+LVS KFGAS +++ENN+ NFTA+ N VLIPVT LP L
 Sbjct 121 NKGIKYLITYVWQDNDNVTLVSSKFGASQVEMLAENNHH--NFTASTNRSVLIPVTSPLKL 178

Query 234 ARSPSDGRKGGIR-LPVIIGISLGCTLLVLVLA VLLVYVYCLMKTLNRSASSAETADKL 292
 + S+GRK + L +IIGISLG +LVL + LVVYVCLMK LNRS SS+ETADKL
 Sbjct 179 DQPSSNGRKSSSQNIALI IIGISLGS AFFILVITLSLVVYCLMKRNLNRSTSSSETADKL 238

Query 293 LSGVSGYVSKPTMYETDAIMEATMNLSEQCKIGESVYKANIEGKVLA VKRKFEDVTEELK 352
 LSGVSGYVSKPTMYE DAIME TMNLS+ CKIGESVYKANI+G+VLA V+ K+D +EELK
 Sbjct 239 LSGVSGYVSKPTMYEIDAIMEGTINLSDNCKIGESVYKANIDGRVLA VKKIKKDASEELK 298

Query 353 ILQKVNHNGLVKL MGVSSDNDGNCFV VYE AENGSL 387
 ILQKVNHNGLVKL MGVSSDNDGNCF+VYE AENGSL
 Sbjct 299 ILQKVNHNGLVKL MGVSSDNDGNCFLV YEAENGSL 333

>ref|XP_002468236.1| hypothetical protein SORBIDRAFT_01g042230 [Sorghum bicolor]
 gb|EER95234.1| hypothetical protein SORBIDRAFT_01g042230 [Sorghum bicolor]
 Length=631

Gene ID: 8085264 SORBIDRAFT_01g042230 | hypothetical protein [Sorghum bicolor]
 (10 or fewer PubMed links)

Score = 441 bits (1133), Expect = 2e-121, Method: Compositional matrix adjust.
 Identities = 256/589 (43%), Positives = 352/589 (59%), Gaps = 57/589 (9%)

Query 32 QDNRTNFSCP-----SDSPPCSTETYIYAQSPNFLSLTNISNIFDTSPLSIARASNL 84
 QDN TN++ P S SPP C+TYV Y QSP + L +IS++F TS IA A+ L
 Sbjct 22 QDN-TNYTVEPAQFACNVSSSSPPCTDYVYRTQSPGYQDLGSISIDLFGTSQARIASANGL 80

Query 85 EPMDDKLVKDQVLLPVPT-CGCTGNRSFANISYEINQGDSFYFVATTSYENLTNWRAVMD 143
 D L Q LLVPV+ CGCTG SFAN++Y I QGD+F+ +A SYENLT ++ +
 Sbjct 81 SSEDGVLQPGQPLLVPVSKCGCTGWSFANVTPYIRQGDTFFNLARVSYENLTLYQLIQN 140

Query 144 LNPVLSQNKLPIGIQVVFPLFCCKCP SKNQLDKEIKYLITYVWKPGDNVSLVSKFGASPE 203
 LNP P L +G +V PLFC+C+P+ E ITYVW+ GD +S VS + +
 Sbjct 141 LNP RSPVPTSLQVGQEVTPLFCRC PAP---AERSSFITYVWQAGDTMSQVSKLMNTTED 196

Query 204 DIMSENNYQGNFTAAN--NLPVLIPVTRLVPL----ARSPSDGRKGGIRLPVIIGISLG 256
 +I NN + +A+ P+LIPV + P L A S DG+ R VIIG S+
 Sbjct 197 EIAEANNVTSSASASLVLQGPMLI PVQQRPRLLPHYAA SAGDGKS RWRRAVII GASVS 256

Query 257 CTLLVVLVLA VLLVYVYCLK-----MKTLNRSASSAE----- 287
 + V+ LA L V + L+ M+ +R A + +
 Sbjct 257 GS--VVVALAALFVAILALR RYRKPKPSMRLGS RFAVNTKLTWSRNQFGHDSNSFAHMMKL 314

Query 288 TADKLLSGVSGYVSKPTMYETDAIMEATMNLSEQCKIGESVYKANIEGKVLA VKRKFEDV 347
 KLL+GVS + +KP ++ +IMEATMNL E+C KIG + Y-A ++G+V AVK K DV
 Sbjct 315 KGKGLLTGVSEFIDKPIIFLEEEIMEATMNLDERCKIGSTYYRAKLDGEVFAVKPAKGDV 374

Query 348 TEELKILOQKVNHNGLVKL MGVSSDNDGN-CFV VYE AENGSL DEWLFSKSCSDTSNSR-- 404
 + ELK+Q VNH NL+KL G+S DG+ F+VYE+AE GS LD+WL+ K S +S
 Sbjct 375 SAELKMMQMVNHNALI KLAGISIGTDGYAFLVYEF AEGS LDKWLYQKPPS ALPSSCC 434

Query 405 --ASLTWCQRISMAVDVAMGLQYMH EAYPRIVHRDITSSNILLDSNFKAKIANFSMAR- 461
 A+L+W QR+S+A+DVA GL YMHEH P +VH DI + NILL + F+ K+I F+ S+A+
 Sbjct 435 TVATLSWGQRLSIALDVANGLLYHM EHTQPSMVHGDIRARNILLTAEFRTKISGFSLAKP 494

Query 462 TFTNPMPM P KIDVFAFGVVLIELLTGRKAMTTKENG VVMLWKDIW KIFDQEENREERLKK 521
 + D VFAFG+L+ELL+GR+AM+ + E+ MLW+I+ D+ RE +L K
 Sbjct 495 ATADAATSSDVFAGL LLELLPSGR RAMEARVGSEIGMLWREIRGVLDAGDKREAKLGK 554

Query 522 WMDPKLESYYPIDYALSLASLAVNCTADKSLSRPTIAEVLSISSLTQP 570
 WMDP L S Y +D ALSLA +A CT D + RP + E+V SLS+L QP
 Sbjct 555 WMDPALGSEYHMDAALSLAGMARACTEDDAARRPNMTEVVFSLSLVQP 603

>emb|CA002953.1| LysM-domain containing receptor-like kinase [Medicago truncatula]
 var. truncatula]
 Length=313

Score = 436 bits (1120), Expect = 6e-120, Method: Compositional matrix adjust.

Identities = 216/315 (68%), Positives = 255/315 (80%), Gaps = 3/315 (0%)

Query 54	YIAQSPNFLSLTNISNIFDTSPSIARASNLEPMDDKLVQDQVLLVPVTCGCTGNRSFAN Y AQSPNFLSL+NIS+IF+ SPL IA+ASN+E D KL+ DQ+LLVPVTCGCT N SFAN	113
Sbjct 1	YRAQSPNFLSLNSNISDIFNLSPRLIAKASNIEADKKLIPDQLLLVPVTCGCTKNHSFAN	60
Query 114	ISYEINQGDSFYFVATTSYENLTNWRAVMDLNPLSPNKLPIGIQVVFPFLFKCPSKNQL I+Y I QGD+F+ ++ TSY+NLTN+ + NP LSP LP+ +V PLFKCPSKNQL	173
Sbjct 61	ITYSIKQGDNNFFILSITSYQNLNTYLEFKFNFPNLSPTLLPLDTKVSVPFLFKCPSKNQL	120
Query 174	DKEIKYLITYWVKPGDNVSLVSDSKFGASPEDIMSENNYQGNFTAANNLPVLIPVTRLVPL +K IKYLITYVW+ DNV+LVS KFGAS ++++ENN+ NFTA+ N VLIPVT LP L	233
Sbjct 121	NKGIKYLITYWQDNDNVTLVSSKFGASQVEMLAENN--NFTASTNRSLVLPVTSPLKL	178
Query 234	ARSPSDGRKGGIR-LPVIIGISLGCTLVLVLAVALVYVYCLMKTLNRSASSAETADKL + S+GRK + L +IIGISLG +LVL + LVVYVCLMK LNRS SS+ETADKL	292
Sbjct 179	DQPSSNGRKSSSNLALIIIGISLGSAFFILVLTLSLVYVYCLMKRNLNRSTSSSETADKL	238
Query 293	LSGVSGYVSKPTMYE DAIMEATMNLSEQCKIGESVYKANIEGKVLAVKRFKEDVTEELK LSGVSGYVSKPTMYE DAIME TMNLS+ CKIGESVYKANI+G+VLAVK+ K+D +EELK	352
Sbjct 239	LSGVSGYVSKPTMYEIDAIMEGTNNLSDNCKIGESVYKANIDGRVLAVKKIKKDASEELK	298
Query 353	ILQKVNHNGLVKLMG 367	
Sbjct 299	ILQKVNHNGLVKLMG 313	

>**emb|CA002964.1|** LysM-domain containing receptor-like kinase [Medicago truncatula var. truncatula]
emb|CA002968.1| LysM-domain containing receptor-like kinase [Medicago truncatula var. truncatula]
Length=311

Score = 433 bits (1113), Expect = 4e-119, Method: Compositional matrix adjust.
Identities = 215/313 (68%), Positives = 254/313 (81%), Gaps = 3/313 (0%)

Query 54	YIAQSPNFLSLTNISNIFDTSPSIARASNLEPMDDKLVQDQVLLVPVTCGCTGNRSFAN Y AQSPNFLSL+NIS+IF+ SPL IA+ASN+E D KL+ DQ+LLVPVTCGCT N SFAN	113
Sbjct 1	YRAQSPNFLSLNSNISDIFNLSPRLIAKASNIEADKKLIPDQLLLVPVTCGCTKNHSFAN	60
Query 114	ISYEINQGDSFYFVATTSYENLTNWRAVMDLNPLSPNKLPIGIQVVFPFLFKCPSKNQL I+Y I QGD+F+ ++ TSY+NLTN+ + NP LSP LP+ +V PLFKCPSKNQL	173
Sbjct 61	ITYSIKQGDNNFFILSITSYQNLNTYLEFKFNFPNLSPTLLPLDTKVSVPFLFKCPSKNQL	120
Query 174	DKEIKYLITYWVKPGDNVSLVSDSKFGASPEDIMSENNYQGNFTAANNLPVLIPVTRLVPL +K IKYLITYVW+ DNV+LVS KFGAS ++++ENN+ NFTA+ N VLIPVT LP L	233
Sbjct 121	NKGIKYLITYWQDNDNVTLVSSKFGASQVEMLAENN--NFTASTNRSLVLPVTSPLKL	178
Query 234	ARSPSDGRKGGIR-LPVIIGISLGCTLVLVLAVALVYVYCLMKTLNRSASSAETADKL + S+GRK + L +IIGISLG +LVL + LVVYVCLMK LNRS SS+ETADKL	292
Sbjct 179	DQPSSNGRKSSSNLALIIIGISLGSAFFILVLTLSLVYVYCLMKRNLNRSTSSSETADKL	238
Query 293	LSGVSGYVSKPTMYE DAIMEATMNLSEQCKIGESVYKANIEGKVLAVKRFKEDVTEELK LSGVSGYVSKPTMYE DAIME TMNLS+ CKIGESVYKANI+G+VLAVK+ K+D +EELK	352
Sbjct 239	LSGVSGYVSKPTMYEIDAIMEGTNNLSDNCKIGESVYKANIDGRVLAVKKIKKDASEELK	298
Query 353	ILQKVNHNGLVKL 365	
Sbjct 299	ILQKVNHNGLVKL 311	

>**emb|CA002944.1|** LysM-domain containing receptor-like kinase [Medicago truncatula var. truncatula]
Length=307

Score = 427 bits (1097), Expect = 2e-117, Method: Compositional matrix adjust.
Identities = 211/309 (68%), Positives = 250/309 (80%), Gaps = 3/309 (0%)

Query 54	YIAQSPNFLSLTNISNIFDTSPSIARASNLEPMDDKLVQDQVLLVPVTCGCTGNRSFAN Y AQSPNFLSL+NIS+IF+ SPL IA+ASN+E D KL+ DQ+LLVPVTCGCT N SFAN	113
Sbjct 1	YRAQSPNFLSLNSNISDIFNLSPRLIAKASNIEADKKLIPDQLLLVPVTCGCTKNHSFAN	60
Query 114	ISYEINQGDSFYFVATTSYENLTNWRAVMDLNPLSPNKLPIGIQVVFPFLFKCPSKNQL I+Y I QGD+F+ ++ TSY+NLTN+ + NP LSP LP+ +V PLFKCPSKNQL	173
Sbjct 61	ITYSIKQGDNNFFILSITSYQNLNTYLEFKFNFPNLSPTLLPLDTKVSVPFLFKCPSKNQL	120
Query 174	DKEIKYLITYWVKPGDNVSLVSDSKFGASPEDIMSENNYQGNFTAANNLPVLIPVTRLVPL +K IKYLITYVW+ DNV+LVS KFGAS ++++ENN+ NFTA+ N VLIPVT LP L	233
Sbjct 121	NKGIKYLITYWQDNDNVTLVSSKFGASQVEMLAENN--NFTASTNRSLVLPVTSPLKL	178
Query 234	ARSPSDGRKGGIR-LPVIIGISLGCTLVLVLAVALVYVYCLMKTLNRSASSAETADKL + S+GRK + L +IIGISLG +LVL + LVVYVCLMK LNRS SS+ETADKL	292
Sbjct 179	DQPSSNGRKSSSNLALIIIGISLGSAFFILVLTLSLVYVYCLMKRNLNRSTSSSETADKL	238
Query 293	LSGVSGYVSKPTMYE DAIMEATMNLSEQCKIGESVYKANIEGKVLAVKRFKEDVTEELK LSGVSGYVSKPTMYE DAIME TMNLS+ CKIGESVYKANI+G+VLAVK+ K+D +EELK	352
Sbjct 239	LSGVSGYVSKPTMYEIDAIMEGTNNLSDNCKIGESVYKANIDGRVLAVKKIKKDASEELK	298
Query 353	ILQKVNHNHGN 361	
Sbjct 299	ILQKVNHNHGN 307	

>**gb|AAM19130.1|AC103891.10** Putative protein kinase [Oryza sativa Japonica Group]
gb|ABF94815.1| Protein kinase domain containing protein [Oryza sativa (japonica cultivar-group)]
gb|EAZ26175.1| hypothetical protein OsJ_10042 [Oryza sativa Japonica Group]
Length=624

Score = 426 bits (1096), Expect = 3e-117, Method: Compositional matrix adjust.
Identities = 251/600 (41%), Positives = 355/600 (59%), Gaps = 43/600 (7%)

Query 10	LHSQILCLVIMLFNSTNIVAQSQQDNRT---NFSCPSDSPSCTYVTYIAQSPNFLSLT + + LC++ ++ + + + T + C + P C+T+V Y QSPF L +	65
Sbjct 1	MEHKGLCILAVVIAFQLLAGEAVTATARARRFACNVSA--CDTFVVYRTQSPGFLDLG	58
Query 66	NISNIFDTSPSIARASNLEPMDDKLVQDQVLLVPVTCGCTGNRSFANISYEINQGDSFY NIS+ + F S IA A+ L D L+ Q LLVPV CGCTG RSFAN+ + Y I D+F+	125

Objct	59	NISDLFGVSRALIASANKLTTEDGVLLPGQPLLVPKCGCTGARSFANVTYPIRPRDTFF	118
Query	126	FVATTSYEENLTNWRAVMMDLNPNVLSPNPKLPIGIQVVFPFLCKCPSKNQLDKEIKYLITYVW +A T++ENLT++ V +LNP +L +FV PLFC+C++ +L + L+TYW	185
Objct	119	GLAVTAFAENLTDFLVLEELNPAAEATRLEPWQEVVVPLFCRCPTREELSGSLLVTVWW	178
Query	186	KPGDNVSLVSDKFGASPEDIMSENNYQGNFTAANNLPVLIPVTRLP-----VLARSP +PGD+VS+VS AS +I + N N T A PVLIPV++ P +A P	237
Objct	179	QPDDVSVSALMNASAAAASNGVAGNSTFATGQPVLIPVSPQPPRFPPPLYGAIAADP	238
Query	238	SDG--RKGGIRLPVIIGISLGCTLVLLVLAFLVLYVYCLKM-----KTLNRS G R G I I G + C VL A+L Y K K+LNR	282
Objct	239	GAGKHRHGIIVATSIAGSFVACA--VLCTAILAYRRYKKAPVKHSPKLSWTKSINRF	296
Query	283	ASSAETA-----DKLLSGVSGYVSKPPTMYETDAIMEATMNLSEQCKIGESVYKANIEGK S++ A DKL+ VS ++ KP ++ + IMEATMNL EQCK+G S Y+AN+E +	336
Objct	297	DSNSSIARMINGGDKLLTTSVQFIDKPIIFREEEIMEATMNLDEQCKLGSSYYRANLERE	356
Query	337	VLAJKRFKEDVTEELKILQKVNHGNLVKLMGVSSNDNGN-CFVVEYAENGSLDEWLFSK V AVK K +V EL++Q VNHL NL K G+S DG+ F+Y+E+AE GSLL+WL+ K	395
Objct	357	VFAVPAKGNVAGELRMMQMVNHNLTLAGISIGADGDYAFLVYEFAEKGSLSDKWLYQK	416
Query	396	SCSDTSNSR--ASLTWCQRISMAVDVAMGLOQMHEAYPRIVHRDITSSNILLDSNFKAK +S A+L+W QR+ +A+DVA GL Y+HEH P +VH D+ +NILL + F+AK	453
Objct	417	PPCSQPSSSSVATLSWDQRLGIALDVANGLLYLHEHTQPSMVHGDVRARNILLTAGFRAK	476
Query	454	IANFSMAR--TFTNPMPMKIDVFAFGVVLIELLTGRKAMTTKENGEEVVMLWKDIWKFQDQ ++NFS+A+ + DVFAFG++L+ELL+GR+A+ + E+ ML +I + D	511
Objct	477	LSNFSLAKPAAMVDAATSSDVFAGLILLLELLSGRRAVEARVGEIGMLRTIEIRTVLDA	536
Query	512	-EENREERLKKWMDPKLESYYPIDYALSLASLAVNCTADKSLRPTIAEIVLSSLTQP + R +L+KWMDP L Y +D ALSLA +A CT + + RP +AEI SLS+L QP	570
Objct	537	GGDKRAAKLKRKWDPTLGEYGVDAALSLAGMARACTEEDAARRPKMAEIAFSLSVLGQP	596

>gb|EAY89155.1| hypothetical protein OsI_10648 [Oryza sativa Indica Group]
Length=624

Score =	426 bits (1094), Expect = 6e-117, Method: Compositional matrix adjust.	
Identities =	251/600 (41%), Positives = 355/600 (59%), Gaps = 43/600 (7%)	
Query	10 LHSQILCLVIMLFSTNIVAQSQQDNRT---NFSCPSDSSPPSETYVTVYIAQSPNFLSLT + + LC++ ++ + + + T +C +P C+T+V Y QSP FL L	65
Objct	1 MEHKGLCILAVVIAFQQLAGGQAVTDATARARRFACNVSAP--CDTFVVYRTQSPGFLDLG	58
Query	66 NISNIFDTPLSIIASRNLEPMDDKLVRDQVLLPVTCGCTGNRSFANISYEINQGDSFY NIS++F S IA A+ L D L+ Q LLVPV CGCTG RSFAN+Y I D+F+	125
Objct	59 NISDLFGVSRALIASANKLTTEDGVLLPGQPLLVPKCGCTGARSFANVTYPIRPRDTFF	118
Query	126 FVATTSYEENLTNWRAVMMDLNPNVLSPNPKLPIGIQVVFPFLCKCPSKNQLDKEIKYLITYVW +A T++ENLT++ V +LNP +L +FV PLFC+C++ +L + L+TYW	185
Objct	119 GLAVTAFAENLTDFLVLEELNPAAEATRLEPWQEVVVPLFCRCPTREELSGSLLVTVWW	178
Query	186 KPGDNVSLVSDKFGASPEDIMSENNYQGNFTAANNLPVLIPVTRLP-----VLARSP +PGD+VS+VS AS +I + N N T A PVLIPV++ P +A P	237
Objct	179 QPDDVSVSALMNASAAAASNGVAGNSTFATGQPVLIPVSPQPPRFPPPLYGAIAADP	238
Query	238 SDG--RKGGIRLPVIIGISLGCTLVLLVLAFLVLYVYCLKM-----KTLNRS G R G I I G + C VL A+L Y K K+LNR	282
Objct	239 GAGKHRHGIIVATSIAGSFVACA--VLCTAILAYRRYKKAPVKHSPKLSWTKSINRF	296
Query	283 ASSAETA-----DKLLSGVSGYVSKPPTMYETDAIMEATMNLSEQCKIGESVYKANIEGK S++ A DKL+ VS ++ KP ++ + IMEATMNL EQCK+G S Y+AN+E +	336
Objct	297 DSNSSIARMINGGDKLLTTSVQFIDKPIIFREEEIMEATMNLDEQCKLGSSYYRANLERE	356
Query	337 VLAJKRFKEDVTEELKILQKVNHGNLVKLMGVSSNDNGN-CFVVEYAENGSLDEWLFSK V AVK K +V EL++Q VNHL NL K G+S DG+ F+Y+E+AE GSLL+WL+ K	395
Objct	357 VFAVPAKGNVAGELRMMQMVNHNLTLAGISIGADGDYAFLVYEFAEKGSLSDKWLYQK	416
Query	396 SCSDTSNSR--ASLTWCQRISMAVDVAMGLOQMHEAYPRIVHRDITSSNILLDSNFKAK +S A+L+W QR+ +A+DVA GL Y+HEH P +VH D+ +NILL + F+AK	453
Objct	417 PPCSQPSSSSVATLSWDQRLGIALDVANGLLYLHEHTQPSMVHGDVRARNILLTAGFRAK	476
Query	454 IANFSMAR--TFTNPMPMKIDVFAFGVVLIELLTGRKAMTTKENGEEVVMLWKDIWKFQDQ ++NFS+A+ + DVFAFG++L+ELL+GR+A+ + E+ ML +I + D	511
Objct	477 LSNFSLAKPAATVDAATSSDVFAGLILLLELLSGRRAVEARVGEIGMLRTIEIRTVLDA	536
Query	512 -EENREERLKKWMDPKLESYYPIDYALSLASLAVNCTADKSLRPTIAEIVLSSLTQP + R +L+KWMDP L Y +D ALSLA +A CT + + RP +AEI SLS+L QP	570
Objct	537 GGDKRAAKLKRKWDPTLGEYGVDAALSLAGMARACTEEDAARRPKMAEIAFSLSVLGQP	596

>emb|CAO02946.1| LysM-domain containing receptor-like kinase [Medicago truncatula var. truncatula]
Length=305

Score =	422 bits (1085), Expect = 6e-116, Method: Compositional matrix adjust.	
Identities =	209/307 (68%), Positives = 248/307 (80%), Gaps = 3/307 (0%)	
Query	54 YIAQSPNFLSLTNISNIFDTPLSIIASRNLEPMDDKLVRDQVLLPVTCGCTGNRSFAN Y AQSQPNFLSL+NIS+IF+ SPL IA+ASN+E D KL+ DQ+LLVPVTCGCT N SFAN	113
Objct	1 YRAQSPNFLSLNISDIFNLSPLRIAKASNIEADKKLIPDQILLPVTCGCTKNHSFAN	60
Query	114 ISYEINQGDSFYFVATTSYEENLTNWRAVMMDLNPNVLSPNPKLPIGIQVVFPFLCKCP SKNQL I+Y I QGD+F+ ++ TSY+NLTN+ + NP LSP LP+ +V PLFCCKCP SKNQL	173
Objct	61 ITYSIKQGDNFFLTSITSYQNLTNTYLEFKNFPNLSPTLLPDTKVSVPFLCKCP SKNQL	120
Query	174 DKEIKYLITYVWKPGDNVSLVSDKFGASPEDIMSENNYQGNFTAANNLPVLIPVTRLPVL +K IKYLITYW+ DNV+LVS KFGAS +++ENN+ NFTA+ N VLIVP TL L	233
Objct	121 NKGKYLITYVWQDNDNTLVSSKFGASQVEMLAENN--NFTASTNRSLVLIPTVSLPKL	178
Query	234 ARSPSDGRKGIR-LPVIIGISLGCTLVLLVLAFLVLYVYCLMKTLNRSASSAETADKL + S+GRK + L +IIGISLG +LVL + LVVYCLMK LNRS SS+ETADKL	292
Objct	179 DQPSNSGRKSSQNLALIIGISLGSAFFILVLTSLVYVYCLMKRKLNRSTSSSETADKL	238
Query	293 LSGVSGYVSKPTMYE DAIME TMNLS+ CKIGESVYKANI+G+VLAVK+ K+D +EELK	352
Objct	239 LSGVSGYVSKPTMYEIDAIMEGTMLSDNCKIGESVYKANIDGRVLAVKIKKDAEELK	298

Query 353 ILQKVNH 359
 Sbjct 299 ILQKVNH 305

>emb|CA002962.1| LysM-domain containing receptor-like kinase [Medicago truncatula]
 var. truncatula]
 Length=304

Score = 418 bits (1075), Expect = 9e-115, Method: Compositional matrix adjust.
 Identities = 208/306 (67%), Positives = 247/306 (80%), Gaps = 3/306 (0%)

Query 54	YIAQSPNFLSLTNISNIFDTSPLSIARASNLEPMDDKLVKDQVLLVPVTCGCTGNRSFAN	113
Sbjct 1	YRAQSPNFLSLNSNISDIFNLSPLRRIAKASNIEAEDKKLIPDQLLVPVTCGCTKNHSFAN	60
Query 114	ISYEINQGDSFYFVATTSYENLTNWRAVMMDLNPNLSPNKLPIGIQVVFPLFCCKPSKNQL	173
Sbjct 61	I+Y I QGD+F+ ++ TSY+NLTN+ + NP LSP LP+ +V PLFCCKPSKNQL	120
Query 174	DKEIKYLITYVWKPGDNVSLVSDKFGASPEDIMSENNYGCQNFTAANNLPLVLIPTRLPVL	233
Sbjct 121	+K IKYLITYW+ DNV+LVS KFGAS +--+ENN+ NFTA+ N VLIPVT LP L	178
Query 234	NKGIGYLITYVWQDNDNVTLVSSKFGASQVEMLAENN--NFTASTNRSVLIPVTSLPKL	238
Sbjct 179	ARSPSDGRKGGIR-LPVIIGISLCTLLVVLAVLLVYVYCLERMKTLNRSASETADKL	292
	+ S+GRK + L +IIGISLG +LVL + LVVYVYCLERMK LNRS SS+ETADKL	
Query 293	DQPSSNGRKSSSQNLALIIGISLGSAFFILVLTSLVYVYCLMKRKLNRSTSSSETADKL	238
Sbjct 239	LSGVSGYVSKPTMYEIDAIMEGTMNLSDNCKIGESVYKANIDGRVLAVRKIKKDASEELK	298
Query 353	LSGVSGYVSKPTMYEIDAIMEGTMNLSDNCKIGESVYKANIDGRVLAVRKIKKDASEELK	352
Sbjct 299	ILQKVN 358	
Sbjct 299	ILQKVN 304	

>ref|XP_002517029.1| Serine-threonine protein kinase, plant-type, putative [Ricinus communis]
 gb|EEF45192.1| Serine-threonine protein kinase, plant-type, putative [Ricinus communis]
 Length=615

Gene ID: 8280185 RCOM_0909430 | serine-threonine protein kinase, plant-type, putative [Ricinus communis]

Score = 366 bits (939), Expect = 5e-99, Method: Compositional matrix adjust.
 Identities = 216/566 (38%), Positives = 324/566 (57%), Gaps = 65/566 (11%)

Query 48	CETYVTYIAQSPNFLSLTNISNIFDTSPLSIARASNLEPMDDKLVKDQVLLVPVTCGC--	105
Sbjct 44	CTY Y A +PNFL L ++ ++F S L I+ SN+ L +Q L VP++C C	103
Query 106	--TGCRSFANISYEINQGDSFYFVATTSYENLTNWRAVMMDLNPNLSPNKLPIGIQVVFP	162
Sbjct 104	T N S+AN+SY I +D+F V+TT ++NLT +AV +NP L P L IG +V+FP	163
Query 163	INSTTNLSYANLSYTIKKDDTFYLVSTTQFQNLTQYQAVQVNMPTLVTLLIEQVEIFP	222
Sbjct 164	LFCKCPSKNQLDKEIKYLITYVWKPGDNVSLVSDKFGASPEDIMSENNYGCQNFTAANNLP	219
+FCFKCP++ QL ++ +I+YV++P DN+SLV+ FG ++ I+ N G N +		
VFCKCPNQTQLQNQVNFMISYVQFQPSDNLSLVASSFGTNTQSIVDVN--GNNIQPFDT--		
Query 223	VLPVTRPLPVLARS--PSDGRKGGIRLPVIIGISLGCTLVVLAVLLVYVYCLERMKTL	279
Sbjct 220	+ +PV RLP L++ PS + R +I G++G + +L +I++ + + L	278
IFVPVNRLPQLSPQPVVPSVPTEKERKGLITGLAVGLVCGFLL-ILIIGSWFREGKL		
Query 280	NRSASS-----AETADKLLSGVSGYVSKPTMYEIDAIMEATMNLSEQC	322
Sbjct 279	NR S E KL++ VS + K +++ D + EAT +E	338
NRKSEDEDKKRLRFYKGEKGLEMETKLIADVSDCLDKYRVEFKIDELKEATDGFNFENF		
Query 323	KIGESVYKANIEGKVLAVERKFKEDVTEELKILQKVNHGNLVLGMVSSDN-DGNCFVYI	381
Sbjct 339	I SVYK +I G+ A+K K + EELKILQKVNHGNLVL G +D DG+C++YE	398
LIQGSVYKGSINGQDYAIKKMKWNAYEELKILQKVNHGNLVLLEGFCIDSEDGSCYLIYE		
Query 382	YAENGSLDEWLFSKSCSDTSNSRASLTWCQRISMAVDVAMGLQYMHEHAYPRIVHRDITS	441
Sbjct 399	Y ENGSL WL N L W R+ +A+DVA GLQY+HEH PR+VH+DI S	451
YIENGSLHSLWH-----INKNEKLNWKTRLRIAIDVANGLQYIHEHTRPRVVHKDIKS		
Query 442	SNIILDSNFKAIIANFSMARTFTNPMM-----PKIDVFAFGVVL	480
Sbjct 452	SNIILDS +AKIANF +A++ N + ++DVF+FGVVL	511
SNIILDSMTRAKIANGLAKSGCNAITMHIVGTQGYIAPEYLTGTVVSTRMDVFSFGVVL		
Query 481	IELLTGRKAMTTKENGEVVMLWKDIWKFQD-QEENREERLKKWMDPK-LESYYPIDYALS	538
Sbjct 512	+EL+G++A+ E G V LW + +D EE + +RLK +MD L ++ +	567
LELISGKEAI--DEEGRV--LWAKVSGNWDGNEEKVKRLKGFMDESLLRESCSMESIIH		
Query 539	LASLAVNCTADKSLSRPTIAIEIVSL 564	
Sbjct 568	++AV C RP++ +IV L	593

>ref|XP_002280070.1| PREDICTED: hypothetical protein [Vitis vinifera]
 Length=622

Gene ID: 100264758 LOC100264758 | hypothetical protein LOC100264758
 [Vitis vinifera]

Score = 355 bits (912), Expect = 8e-96, Method: Compositional matrix adjust.
 Identities = 220/589 (37%), Positives = 329/589 (55%), Gaps = 68/589 (11%)

Query 28	AQSQ-QDNRTNFSCPSD-SPPSCETYVTYIAQSPNFLSLTNISNIFDTSPLSIARASNLE	85
Sbjct 27	+Q+Q + N T + C ++ S C T+ Y A SPNFL L +I ++F S L I+ SN+	86
SQAQPEPNATGYPCSANLSSYPCHTFAFYTATSPNFLDLASIGDLFWVSRLMISEPSNIS		
Query 86	PMDDKLVKDQVLLVPVTCGCG----TGCRSFANISYEINQGDSFYFVATTSYENLTNWRA	140
+ LV Q L VP+ C C T S+AN+SY I GD+FY V+T S+ NLT + +		

Subjct	87	SPSNPLVAGQSLFVPLNCSCNSVNTTAISYANLSYTIKSGDTFLVSTFSFLNLTTYY	146
Query	141	VMDLNPVLSPNPKLPIGIVQQVFPFLCKCPSKNQLDKEIKYLITYWVKPGDNVSLVSDKFGA	200
Subjct	147	VEIVNPTLVTDLDVGDKVIFPIFCCKCNETQLRNGVNFLISYVFQPSDNLTVGAASLGS	206
Query	201	SPEDIMSENNYGGQNTAANNLPVLIPVTRLP-----VLARSPSDGRKGIGIRLPVIIGIS	254
Subjct	207	DTASIIDVN--GDNIQPFQT--IFVPVSRLPNISQPNVTASVATSVRKVE-RKGVIIGLA	261
Query	255	LGCTTLLVVLVLAFLVYVYCL--KMKT-----NRSASSAETADKLLSGVSGYV	300
Subjct	262	+G C +L++I + VY + + K+K + R L++ VS +	321
Query	301	SKPTMYETDAIMEATMNLSEQCKIGESVYKANIEGKVLAJKRFKEDVTEELKILQKVNHG	360
Subjct	322	K + Y + + +AT SE+ I SVYK +I+G++ A+K+ K + EELKILQKVNHG	381
Query	361	NLVLMGVSSD-NDGNCFVYYEYAENGSLDEWLFSKSCSDTSNSRASLTWCQRISMADV	419
Subjct	382	NLV+L G D C++VYE+ ENGLS WL + L W R+ +A+DV	434
Query	420	AMGLQYMHEHAYPRIVHRDITSSNILLDSNFKA KIANFSMARTFTNPMM-----	468
Subjct	435	A GLQY+HEH PR+VH+DI SSNILLD N +AKIANF +A++ N +	494
Query	469	-----PKIDVFAFGVVLIELLTGRKAMTTKENGEVVMILWKDIWKFID--QEENRE	516
Subjct	495	+DVF+FGVVL+EL++G++A+ E G V LW I + E+ +	550
Query	517	PEYLAGVVSTRMDVFSFGVVLLELISGKEAV--DEEGRV--LWMSARGILEKDEKVKA	564
Subjct	551	RWMKDWMDEGLLRESCSMSVINVMAVATACTHRDP SKRPSMVDIVYAL	599

>**gb|AAT00791.1|** SYM10-like protein [Galega orientalis]
Length=244

Score =	351 bits (901),	Expect = 2e-94,	Method: Compositional matrix adjust.
Identities =	179/244 (73%),	Positives =	204/244 (83%), Gaps = 3/244 (1%)
Query	223	VLIPVTRLPVLARSPSDGRKGIR-LPVIIGISLGCTLLVVLVLAFLVYVYCLMKTLNR	281
Subjct	1	+LIPVT LP L + S G + LPVIIGISLG + +VL + LVVYCLMKL NR	60
Query	282	SASSAETADKLLSGVSGVSKPMTYETDAIMEATMNLSEQCKIGESVYKANIEGKVLA	341
Subjct	61	S S AETADKLLSGVSGVSKPMTYE D IMEA +LS+QCKIGESVYKANI+ + LAVK	120
Query	342	RFKEDVTEELKILQKVNHGNLVKLMGVSSDNDGNCFVYYEYAENGSLDEWLFSKSCSDTS	401
Subjct	121	+K+D +EELKILQKVNHGNLVKLMGVSSDNDGNCF+VYYEYAENGSL+WLFSD++ S TS	179
Query	402	NS-RASLTWCORISMADVAMGLQYMHEHAYPRIVHRDITSSNILLDSNFKA KIANFSMA	460
Subjct	180	NS +SLTW QRI +A+DVA+GLQYMHEH YPRI+HR IT+SNIL+DSNFKA KIANF	239
Query	461	RTFT 464	
Subjct	240	+T T KTST 243	

>**emb|CBI26350.3|** unnamed protein product [Vitis vinifera]
Length=595

Score =	345 bits (884),	Expect = 1e-92,	Method: Compositional matrix adjust.
Identities =	217/575 (37%),	Positives =	320/575 (55%), Gaps = 67/575 (11%)
Query	28	AQSO-QDNRTNFSCPSD-SPPSCETVVTYIAQSPNFLSLTNISNIFDTSPSLSTARASNLE	85
Subjct	27	+Q+Q + N T + C ++ S C T+ Y A SPNFL L +I +F S L I+ SN+	86
Query	86	PMDDKLQVLDQVLLVTPVTCGC-----TGNRSFANISYEINQGDSFYVATTSYENLTNWRA	140
Subjct	87	+ LV Q L VP+ C C T S+AN+SY I GD+FY V+T S+ NLT + +	146
Query	141	VMDLNPVLSPNPKLPIGIVQQVFPFLCKCPSKNQLDKEIKYLITYWVKPGDNVSLVSDKFGA	200
Subjct	147	V +NP L P L +G +V+F+FCCKC++ QL + +LI+VY++P DN++ V+ G+	206
Query	201	SPEDIMSENNYGGQNTAANNLPVLIPVTRLP-----VLARSPSDGRKGIGIRLPVIIGIS	254
Subjct	207	I+ N G N + +PV+RLP V A + RK R VIIG++	261
Query	255	DTASIIDVN--GDNIQPFQT--IFVPVSRLPNISQPNVTASVATSVRKVE-RKGVIIGLA	261
Subjct	262	LGCTTLLVVLVLAFLVYVYCLMKTLNRSASSAETADKLLSGVSGVSKPMTYEIDV	314
Query	315	MEATMNLSEQCKIGESVYKANIEGKVLAJKRFKEDVTEELKILQKVNHGNLVKLMGVSSD-ND	373
Subjct	309	T SE+ I SVYK +I+G++ A+K+ K + EELKILQKVNHGNLV+L G D D	368
Query	374	TGGFSERSLIQGSVYKGSIDGEYAIKKMKWNAYEELKILQKVNHGNLVRLEGFCIDPED	433
Subjct	369	TMNLSEQCKIGESVYKANIEGKVLAJKRFKEDVTEELKILQKVNHGNLVKLMGVSSD-ND	421
Query	434	ATCYLVYEFVENGSLQSWLH-----GDRDEKLNWKNRLRIAIDVANGLQYIHEHTRPR	472
Subjct	422	IVHRDITSSNILLDSNFKA KIANFSMARTFTNPMM-----PKID +VH+DI SSNILLD N +AKIANF +A++ N +	481
Query	473	VFAFGVVLIELLTGRKAMTTKENGEVVMILWKDIWKFID--QEENREERLKKWMDPK-LES	529
Subjct	482	VF+FGVVL+EL++G++A+ E G V LW I + E+ + +R+K WMD L	537
Query	530	VFSFGVVLLELISGKEAV--DEEGRV--LWMSARGILEKDEVKAKRVKDWMDEGLLRE	564
Subjct	538	YYPIDYALSLASLAVNCTADKSLSRPTIAEIVLSL +D +++ +A CT RP++ +IV +L	572

>**gb|ABR17803.1|** unknown [Picea sitchensis]
 Length=536
 Score = 343 bits (881), Expect = 3e-92, Method: Compositional matrix adjust.
 Identities = 200/516 (38%), Positives = 293/516 (56%), Gaps = 59/516 (11%)

Query 108 NRSFANISYEINQGDSFYFVATTSYENLTNWRAVMIDLNPVLSPNKLPIGLIQVVFPLFCKC 167
 N S AN++Y I GD+FY ++T +ENLT + AV NP L L IG P+ CKC
 Sbjct 3 NYSQANVNTYTIYGCGDTFYLIISTRKFENLTTYPAVEVTNPTLVVTNLQIGSLATIPIRKCKC 62
 Query 168 PSKNQLDKEIKYLITYVWPKCDNVSLVSDKFGASPEDIMSENNYQQNFTAANNLPVLI PV 227
 PS Q+ K LITYV PGD + +S KFGA +++ S N G N T +L+PV
 Sbjct 63 PSNAQVTNGTKMLITYVVHPGDTLLNISQKFGADLQNLKSLN--GINSTLIPYSTLLPV 120
 Query 228 TRLPVLAR-----SPSDGRKGIGIRLPVIIGISLGCTLLVVLVIAVLLVYV 271
 ++ PL+A+ + + GG+ +IG S+G + V+ +A+L+ V
 Sbjct 121 SQKPVLAQPPSPSPPPPPPLVNNATSSGGLHGGAVIGASVGSAAVCIALIFCV 180
 Query 272 YCLKMKTLNRSASS-----AETADKLLSGVSGYVSKPTMYETDAIMEATMNLSE 320
 K ++ ++ S +T KL++G+S V P MY + + +AT N S
 Sbjct 181 VIRKRRSYKQTSISEDQRPPSDVGKTKSKLMTGISDCVENPFMYSIEDLDKATQNFSP 240
 Query 321 QCKIGESVYKANIEGVKVLAVKRFKEDVTEELKILQKVNHGNLVLKMGVSSDNDGNCFVYY 380
 C I SVYK ++G+ A+K K D++ELKILQKVNH NLVKL GV ++G ++VY
 Sbjct 241 LCNIEGSVYKGTLDGRDYAIKLMKGDISQELKILQKVNHNTNLVLEGVCISSEGQSILVY 300
 Query 381 EYAENGSLDEWLFS---KCSCTSNSRASLTWCQRISMAVDVAMGLQYMHEHAYPRIVH 436
 EY EN SL+ WL ++ S S +SL W R+ +A+DVA GLQY+HEH P +VH
 Sbjct 301 EYIENSSLNTWLHDPESENENMSPIGWSSSLPWKTRLQVALDVANGLQYIHEHTTPSVVH 360
 Query 437 RDITSSNILLDSNFKA KIANFSMARTFTNPMM-----PKIDVFA 475
 +DI SSNIILD NF+AKIANF MA++ N + PK+DVFA
 Sbjct 361 KDIKSSNILLDGFRAKTANFGMAKSGINALT KHIMGTQGYMAPEYLADGFVSPKLDVFA 420
 Query 476 FGVVILELLTGRKAMTTKEN---GEVVMLWKDIWKFQDQEENREERLKKWMDPKLESYY 531
 FGVVL+E+++G+A+ + G+ +LW I + + E+ E +L+K+D L++ Y
 Sbjct 421 FGVVLEMISGKEAIVRERGVPLAGKAGLLWTQIRPLLEGED-IEGKLKRVWDRNLQNY 479
 Query 532 PIDYALSLASLAVNCTADKSLSRPTIAEIVLSSL 567
 +D L +A++A C + ++RPT+ EIV LS L
 Sbjct 480 TMDSILGVATIARACVEEDPVARPTLPEIVYKLSNL 515

>**emb|CAN66762.1|** hypothetical protein [Vitis vinifera]
 Length=591
 Score = 338 bits (867), Expect = 1e-90, Method: Compositional matrix adjust.
 Identities = 205/567 (36%), Positives = 314/567 (55%), Gaps = 55/567 (9%)

Query 28 AQSQ-QDNRTNFSCPSD-SPPSCETYVTYIAQSPNFLSLTNISNIFDTSPLSIARASNLE 85
 +Q+Q + N T + C ++ S C T+ Y A SPNFL L +I ++F S L I+ SN+
 Sbjct 27 SQAQPEANATGYPPCSANLSSYPCHTFAFYATATSPNFLDLASIGDLFWVSRLMISEPSNIS 86
 Query 86 PMDDKLVQDQVLLVPVTCGC-----TGNRSFANISYEINQGDSFYFVATTSYENLTNWRA 140
 + LV Q L VP+ C C T S+AN++Y I GD+FY V+T S+ NLT + +
 Sbjct 87 SPSNPLVAGQSLFVPLNCSCNSVNATAISYANLTYTIKSGDTFLVSTFSFLNLTTTYS 146
 Query 141 VMDLNPVLSPNKLPIGLIQVVFPLFKCPSPKNQLDKEIKYLITYVWKGDNVSLVSDKFGA 200
 V +NP L P L +G +V+FP+FKCP++ QL + +LI+V++P DN++ V+ G+
 Sbjct 147 VEIVNPTLVTDLVGDKVFIFCKCPNETQLRNGVNFLISYVFPQSDNLTVGAASLGS 206
 Query 201 SPEDIMSENNYQQNFTAANNLPVLIPTVRLPVLAR-----SPSDGRKGIGIRLPVIIGISL 255
 I+ N G N + +PV+RLP + +SP+ + R IIG+S+
 Sbjct 207 DTASIIVDN--GDNIPQFQT--IFVPVSRPNISQPNVTASPATSVRVERGAIIGLSI 262
 Query 256 G--CTLLVLVLA VLLVYVYCL--KMKT-----NRSASSAETADKLLSGVSGYVS 301
 G C +L++ +L + VY + + K+K + R + L++ VS +
 Sbjct 263 GLGVC GILLVLLGVWVYRHVMVEKIKEIEGDKERPLVGRGSGLKAEEVNLIMADVSDCLD 322
 Query 302 KPTMYETDAIMEATMNLSEQCKIGESVYKANIEGVKVLAVKRFKEDVTEELKILQKVNHGN 361
 K +Y + + +AT SE+ I SVYK +I+G++ A+K+ K + EELKILQKVNHGN
 Sbjct 323 KYK VY GIEELR DATGGFSERSLIQGSVYKGSIDGELYAIKKMKNAYEELKILQKVNHGN 382
 Query 362 LVKLMGVSSD-NDGNCFVYYEYAENGSLDEWLFSKSCSDTSNSRASLTWCQRISMAVDVA 420
 LV+L G D D C++VYE+ ENGL S+L W R+ +A+DVA
 Sbjct 383 LVRLEGFCIDPEDIATCYLVYEFVNGSLQSWLH-----GDRDEKLNWKNRIRIAIDVA 435
 Query 421 MGLOYMHEHAYPRIVHRDITSSNILLDSNFKA KIANFSMARTFTNPMPKIDVFAFGVVL 480
 GLQY+HEH PR+VH+DI SSNIILD N +AKIANF +A++ N +
 Sbjct 436 NGIYQIHEHTRPRVHVHKDIKSNILLDGNMRAKIANFGLAKSGCN-----AIT 483
 Query 481 IELLGRKAMTTKENGEVVMLWKDIWKFQDQEENREERLKKWMDPK-LESYYPIDYAL 537
 + ++ + E G V LW I + E+ + +R+K WMD L +D +
 Sbjct 484 MHIVGTQGKEAVDEEGRV--LWMSARGILEGKDEVKVAKRVKDWMDEGLLRESCSMDSVI 541
 Query 538 SLASLAVNCTADKSLSRPTIAEIVLSL 564
 ++ ++A CT RP++ +IV +L
 Sbjct 542 NVMAVATACTHRDP SKRPSMVDIVYAL 568

>**ref|XP_002311653.1|** predicted protein [Populus trichocarpa]
gb|EEE89020.1| predicted protein [Populus trichocarpa]
 Length=524

Gene ID: 7473444_POPTRDRAFT_564909 | hypothetical protein [Populus trichocarpa]
 (10 or fewer PubMed links)

Score = 324 bits (831), Expect = 2e-86, Method: Compositional matrix adjust.
 Identities = 188/500 (37%), Positives = 281/500 (56%), Gaps = 56/500 (11%)

Query 110 SFANISYEINQGDSFYFVATTSYENLTNWRAVMIDLNPVLSPNKLPIGLIQVVFPLFCKCP 169
 S AN+Y I GD+FY V+T ++NLT ++V NP L P L IG++V+FB+FCCKC
 Sbjct 13 SSANANTYIEAGNTFYIVSTKYFQNLTTTYSQSVELFNPTLIEPELLDIGVEVIFCKCPH 72
 Query 170 KNQLDKEIKYLITYVWKGDNVSLVSDKFGASPEDIMSENN----YQQNFTAANNLPV 224
 + QL ++ YL++VY++P DN+S V+ FG + I+ N Y F N LP L

Sbjct	73	QTQLQNKVNYLVSYVFQPSDNLLSSVASTFGVETQSISDVNGNNIQPYDITFIVPVLQLQL	132
Query	225	I-PVTRLPLVLRSPSDGRKGIRLPIIIGISLGCILLLVLLVLAFLVYVYCLKMK----- P + P A P + G+ + +G+ + LLVL V LK +	277
Sbjct	133	AQPTVVVPSGAPPKEKTERKGVIIGLAVGLGIAGLVLVLSGVWFWYREGVLRKRRDVEKV	192
Query	278	-----TLNRSSAETAD-KLLSGVSYVSPTMYYTDAEATMNLSEQCCKIGESVYK LN + + + L++ VS + K + ++ D + EAT SE C I SV+K	330
Sbjct	193	EKKRMRMLNGGSKGLKDIEVSLMADVSDCLDKYRKFIDELKEATNGFSENCLIEGSVFK	252
Query	331	ANIEGKVLAVKRFKFEDVTEELKILQKVNHNGLVKLMGVSSD-NDGNCFVYVEYAENGSLD +I G+ A+K+ K+ + EELKLQKVNHNGLVKL G D D NC++VYE+ ++GSL	389
Sbjct	253	GSIINGETYAIKKMWNACEELKILQKVNHNGLVKLEGFCIDPFEDANCYLVEFVDGSLH	312
Query	390	EWLFSKSCSDTSNSRASLTWCQRISMAVDVAMGLQYMHAYPRIVHRDITSSNILLDSN WL N + L+W R+ +A-DVA GLQY+HEH PR+VII+DI SSNILLDS+	449
Sbjct	313	SWLH-----RNEKEKLSWKTRLRAVIDVANGLQYIHEHTRPRVVHKDIKSSNILLDSS	365
Query	450	FKAKIANFSMARTFTNPMM-----PKIDVFAFGVWLIELLTLGRK +AKIANF+A+T N + + + +DVF+FGVWL+EL++GR+	488
Sbjct	366	MRAKIANFLAKTCNCNAITMHIVGTQGYIAPEYLADGVVSTRMDVFSFGVVLLELISGRE	425
Query	489	AMTTKENGEBVVMLWKDIWKIFD---QEENREERLKKWNMDPK-LESYYPIDYALSLASLAV A+ E G+V LW + + + +E + +RL WMD LE ++ ++ +++A+	544
Sbjct	426	AI---DEEGKV--LWAEEAIGVLEGNVEEERRKVKRLTAWMDKVLLEESCMESVMNTMAVAI	481
Query	545	NCTADKSLSRPTIAEIVLSSL 564	
Sbjct	482	ACLHRDPKSRSRPSMVDIVYAL 501	

>emb|CA002950.1| LysM-domain containing receptor-like kinase [Medicago truncatula]
var. truncatula
Length=243

Score = 313 bits (801), Expect = 6e-83, Method: Compositional matrix adjust.
Identities = 158/245 (64%), Positives = 191/245 (77%), Gaps = 3/245 (1%)

Query	54	YIAQSPNPLSLTNISNIFDTSPLSIARASNLEPMDDKLVKDQVLLVPVTCGCTGNRSFAN	113
Sbjct	1	YAQSPNPLSLNISDIFNLSPRIAKASNIEADKKLIPDQLLLVPVTCGCTKNHSFAN	60
Query	114	ISYEINQGDSFYFATTYSYENLTNWRAVMIDLNPVLSPNPKLPIGIQVVFFLFCKPCKPSKNQL	173
Sbjct	61	I+Y I QGD+F+ ++ TSY+NLTN+ + NP LSP LP+ +V PLFCKCPSKNQL	120
ITYSIKQGDNFFFILSITSYQNLNTYLEFKFNFPNLSPTLLPDLTKVSVPLFCKCPSKNQL			
Query	174	DKEIKYLITYVWKPGDNVSLSVSDKFGASPEDIMSENYYQGNFTAANNLPLVLIPTVTRLPVL	233
Sbjct	121	+K IKYLYTIVW+ DNRN+LVS KFGAS +--+ENN+ NFTA+--+ VLPVT LPL	178
NKGKIYLITYVWQDNDVNTLVSSKGASQVEMLAENNHH--NFTASTNRSQLPFLSKPFL			
Query	234	ARSPSDGKGGIR+LPVIIIGISLCLTLVVLVLAIVLLVYVYCLMKMTLNRSASSAETADKL	292
Sbjct	179	+ S+GRK + L +IGISLG +LVL + LVVYVCLMK LNRS SS+ETADKL	238
DQPSSNGRKSSSQNLALIIGISLGSAFFILVLTLSLVYVYCLMKRNLNRSTSSSETADKL			
Query	293	LSGVS 297	
Sbjct	239	LSGVS 243	

>gb|EAY87082.1| hypothetical protein OsI_08480 [Oryza sativa Indica Group]
Length=651

Score = 313 bits (801), Expect = 6e-83, Method: Compositional matrix adjust.
Identities = 205/601 (34%), Positives = 310/601 (51%), Gaps = 85/601 (14%)

Query	37	NFSCSPDSSPPSCETVYIAQSPNF-LSLTNIISNIEDTSPSLARIASRNLEPMDDKLVKHQ F+C +++ C Y A L I +F S +A+NL L Q	95
Sbjct	39	GFnCTANATYPCPAYALRAGFVGVPLEFAAIGDLFAASRFVMWAHNNLTS- TSAVLAARQ 97	
Query	96	VLLVPVTCGCTGN--RSFANISYEINQGDSFYFVATTSYENILNTNWRAVMMDLNPVLSPNKL L1LP+ CGC ++A +Y+IN GD+++ V+TT +NLIT ++AV +NP L P L	153
Sbjct	98	PLLVLPLQCQCPSPRSRNAYAPMQYQINAGDTYWIVSTKLQLNLTQYQAVERVNPTLVPTNQ 157	
Query	154	PIGIQVVFPLFCKCPNSNQLDKEIKEYLIWVYWKPGDNVSLSVLDKFGASPEMSENYYQ I V F+FC+C+P+ +L+TYV+PGD++ F ++S N Q	213
Sbjct	158	DIGQIVTFPIFCQCPТА--EDNATALVTYVMQPGDTYASIATAFAVDADQSLVSLNGFEQ 214	
Query	214	NFTAANNLPVLI PVTR-----LPVLAR-----SPSDGRKGIGRLPVII----- ++ +L+P+ R LP + R +P+ P + +	251
Sbjct	215	GTRNLSSPEILPVLRQPVPEWLPIVRRVNNISTTPASPPSNTPAVTWSNNRDGVVTGL 274	
Query	252	GISLGCTLLVLVLAFLVLYVYCLMKMTLNRSSAETADK----- I LG + +L +LL+ ++K R A + + D	291
Sbjct	275	AIGLGVVGGLWLQMILLGCLWRRLKARGRRAEAVASGDGEGGRFTKAASGGGGGGGG 334	
Query	292	--LLSGVSGVYSEKPTMYEFDAIMEATMLNSEQCKIGESVYKANIEGKVLAVKRFKEDVTE L+S +S ++ K +++ + + T ++ I SVYKA I+G+V AVK+ K D E	349
Sbjct	335	RFLVSDISELDRYKVKFVEELESHTGGFDDEHLIQGSVQSYKAYIDGEVFKVMKWDACE 394	
Query	350	ELK1LQKVNHGNLVKLMGVSSNDN-GNCFVVYEAENGSLDEWLFSKCSCTSNSRASLT ELK1LQKVNH NLVKL G +++ G+C+VVEY ENGSLD WL D +R L	408
Sbjct	395	ELK1LQKVNHNSNLVKLEGFCINSETGDCYLVYEYVENGSLDLWLM-----DRDRAR-RLD 448	
Query	409	WCORISMAWDVAMGLQYMHAEHYPRVHRDTISSNILLDSNFKAKIANFSMARTFTNP-- W R +A+D+A GLQY+HEH+PR+VH+DI SSN+LLD +AKIANF +A+T N	466
Sbjct	449	WRARLHIALDLAHLGQYIHEHTWPRVVHKDKISSNVLLDDRMRAKIANFGLAKTGHNAVT 508	
Query	467	-----MMPKIDVFAFGVVLIELLTGRKAMTTKENGEVVMLWKDI-W + K+DVF+A+GVVL+EL+GR+A+ + +GE LW D	506
Sbjct	509	THIVGTQGYIAPEYIADGLTVKMDVFAYGVVLELVSGREAV-SDDSRGE--PLWADADE 565	
Query	507	KIFDQEENR-EERLKKWMDPKL-ESYYPIDYALSLASI LAVNCTADKSLSRPTEIAVLSL ++F E R E R+ WMDP L E P S+ S+A C RP++ ++ +L	564
Sbjct	566	RLFRGRRELEARVAAWMDPALAEQTCPGGSVASVSVAKACLHRDPAKRPSMVDVAYTL 625	
Query	565	S 565	
Sbjct	626	S 626	

>ref|XP_001767824.1| predicted protein [Physcomitrella patens subsp. patens]
 >gb|EDQ67338.1| predicted protein [Physcomitrella patens subsp. patens]
 Length=658

GENE ID: 5931014 PHYPADRAFT_132645 | hypothetical protein
 [Physcomitrella patens subsp. patens] (10 or fewer PubMed links)

Score = 302 bits (774), Expect = 8e-80, Method: Compositional matrix adjust.
 Identities = 211/624 (33%), Positives = 319/624 (51%), Gaps = 84/624 (13%)

Query 26	IVAQSQQDNRTNFSCPSDSPPSCETYVTYIAQSPNFLSLTNISNIFDTSPLSIARASNLE	85
I	AQ Q N + ++C + C+TY Y +LT+I +F+TS IA AS++	
Sbjct 24	ISAQQQYRNTSGYTCGTT--RCQTYAFYRTAGSQS-TLTSIVTFLNTSVEGIATASDVD	80
Query 86	PMDDKLVLKDQ-VLLVPVTCGCTGNRSFANISYEINQGDSFYFVATTSYENLTNWRAVMDL	144
P	D+ L +P+ C C N A S+I GD+Y A +Y+ LT W A+	
Sbjct 81	PNRTIPFNDRDPLYIPLNCSCFNNTFRALTSQKISGDTMYKFANGTYQGLTTWEAISVA	140
Query 145	NPVLSPNKLPIGIQVVFPFLCKPKSKNQLDKEIKLITYVWKEPGDNVSLVSDKFAGSPED	204
NP	+ + +G +V PL C CP+ Q +L+TY P + + +S F +	
Sbjct 141	NPTVIITNMTVGDLVLIPLRCACPTTQRAGSRILLITYSIFPDETLKFISGLFNIPEVE	200
Query 205	IMSENNYQG---NFTAANN---LPVLIPVTRLPVLARS-----SDGRKGGIRLPVI-----	250
+	NN N A LP L+P++ + + P + G +PVI	
Sbjct 201	LQTANNGASSANLAFTTLLVPLPSLVLSTMFKFPSPPPSVEARPGPAPSTLVPPVITNKD	260
Query 251	-----IGISLGCTLLVLVLA VLLVYVYCLKMKT-----LNRSAS-----	284
IGI	G + LA +L V C +K LNR +S	
Sbjct 261	PSKTSMYIYGIVFGG---FGMALIACVLICATVKRYKNIIRKEYENRGLLNRKSSVTDI	318
Query 285	-SAETAD-KLLSGVSGYVS---KPTMYETDAIMEATMNILSEQCKIGESVYKANIEGKVLA	340
S	+TA+ L+SG++ K T + + + AT + SE +I SV+ A + G +A+	
Sbjct 319	DSLDTANSSLVSGMTDLFGCDKLTKEFSEYELDTATNHFSEDNRIQGSVFLAKLNGSFVAI	378
Query 341	KRFKEDVTEELKILQKVNHGNLVKLMGV---SSNDG---NCFVYYEAENGSLDEWLFSKS	396
KR	K ++++ELKIL +V+HGN+VRL+G+ D+DG N ++VYEAENGSL + L +	
Sbjct 379	KRMKGNSDELKILSLSQVHHGNVVKLVGMARDSGRSENLYIIVYEAENGSLSDCLHHQM	438
Query 397	CSDTSNSRAS---LTWCQRISMAVDVAMGLQYMHEAYPRIVHRDITSSNILLDSNFKAK	453
TSN	S L W R+ +AVD+A GL+Y+H+ P +VH+D+ SSNILLD NF+AK	
Sbjct 439	AYPTSNFSRSVGLLIWNTRMQIAVDIASGLEYLHNNTNPSLVHKDVKSSNILLDKNFRAK	498
Query 454	IANFSMARTFTN---PM-----PKIDVFAFGVVLIELLTGR-----	487
+ANF	MA+ + P+M+ K DVF+FGVV+ELL+GR	
Sbjct 499	VANFGMAKPADSGEPGPMLTEHIVGTQGYMAPEYLEHGLVSTRADVSFGVVILLELLSGR	558
Query 488	KAMTTKENGEVVMLWKDIWKFQDENREERLKKWMDPKLESYYPIDYALSLASLAVNCT	547
+A+	GE ML I + ++ + +L WMDP+L++ YP D ALS+A LA +C	
Sbjct 559	EAICNDGGGEFTMLSATISNVLSQDD-QMAKLIQAWMDPRLQNAYPSDIALSVAIILAKSCV	617
Query 548	ADKSLSRPTIAEIVLSSLTQPS	571
SRP	+ I + LS ++ S	
Sbjct 618	ETDPDRSRPDMKQISFALKMSSAS	641

>dbj|BAI79278.1| LysM type receptor kinase [Lotus japonicus]
 Length=666

Score = 297 bits (761), Expect = 2e-78, Method: Compositional matrix adjust.
 Identities = 189/631 (29%), Positives = 327/631 (51%), Gaps = 88/631 (13%)

Query 14	IILCLVIMLFSTNIVA-OSQODD---NRTNFSCPS-----DSPPSCETYVTYIAQSPN	60
+L	++I+ FS I + Q+Q+ N C + +S SC+Y+T+ + SP	
Sbjct 18	LLVMVIISFSHMIPSTQAQQEYVNNKQLDCDTQYNTTYGNVCSNTSCQSYLTFKSSSPE	77
Query 61	FSLTNISNIFDTSPLSIARASNLEPMDDKLVKDQVLLVPVTCGCTGNRSFANISYEINQ	120
+	++IS + ++P +A++N+ + ++ D ++ VPVTC C+G R N +Y + +	
Sbjct 78	YNTPSSISYLLNSTPSLVAKSNNITDV-PIITDTMVTPVPTCSCSGGRYQHNATYNLKK	136
Query 121	-GDSFYFVATTSYENLTNWRAVMDLNPVLPSPNKLPIGIVQVVFPLFCPKCPSKNQLDKEIKY	179
G+++	+A +Y++LT +A+M NP + N L G + PL C CP+K Q D KY	
Sbjct 137	TGETYFSIANNTYQSLTTCQALMAQNPYDAKN-LFAGDDLHVPLRCACPTKKQSDAGFKY	195
Query 180	LITYVWKPGDNVSLVSDKFGASPDIMSENNYQNFATAANLPLVLPVTRLP-----	231
L+TY+	G++ +++ FG + ++ N +P+I+P+ P	
Sbjct 196	LITYLVSQGESPSDIAEIFGVDTQSVDLNELDKSLSVFFYFTLVLVPLKTEPPARLQIAA	255
Query 232	-----VLARSPSGRKGGIRLPIIIGISLGRGCTLLVLVLA VLLVYVYCL-----	274
+	+ VI+G++G + ++V LIV+ C	
Sbjct 256	SPESPAPPAGNDSSSSKKWVIVGVTGVAVCLVV--ALLVFFLCFYNRRRQPAPPP	313
Query 275	-----KMKTLNRSASSAETADKLLSGVSGYVSKPMTYETDAIMEATMNILSEQCKIG	325
+K	+++ + E+ GV + T Y+ I AT SE+ KI	
Sbjct 314	VSVKDFPDASVKMSETTPTTESWSLSSEGVRVYAIESTAYKFDIQTATKFFSEENKIK	373
Query 326	ESVYKANIEGKVLA VKRKFEDVTEELKILQKVNHGNLVKLMGVSSDNDGNCFVYYEAEN	385
SVY+A+	+ G AVK DV+ E+ L++NH N++L G + GN ++VY+E+AEN	
Sbjct 374	GSVYRASFKGDDAAVKILNGDVSAEINLLKRINHANIIRLSGFCV-HKGNTYLVYEAEN	432
Query 386	GSILDEWLFSKSCSDTSNSRASLTWCQRISMAVDVAMGLQYMHEAYPRIVHRDITSSNIL	445
SLL+WL	S S SL+W QR+ +A DVA L Y+H + P +H++ S N+L	
Sbjct 433	DSDLDDWLHSDDKQYQNS--VSLSWMQRVQIAYDADALNLYLHNNTNPIHIHKNLKGNSVL	489
Query 446	LDSNFKA KIANFSMARTFTNP-----MMPKIDVFAFG	477
LD	F+AK+NF +AR + + PK+DVFAFG	
Sbjct 490	LDGKFRAKVSNFGLARVMEDQGEDGGFQMTRHVVGTQGYMPPEYIESGLITPKMDVFAFG	549
Query 478	VVLLLTGRKAMTKEN---GEVVMLWKDIWKFQDENREERLKKWMDPKLESYYPID	534
VV++ELL+GR+A	++ E GE ML + + + +N + +L +MDP L YP+D	
Sbjct 550	VVMLELLSGREATSSGEKNGLGENKMLSETVNHLV-EGDNVRDQLRGFMPTLREYPLD	608
Query 535	YALSLASLAVNC TADKSLSRPTIAEIVLSSL	565
A	S+A +A C A SRP I+E+++LS	
Sbjct 609	LAYSMAEIAKRCVAHDLNSRPNISEVIMTLS	639

>ref|XP_002326901.1| predicted protein [Populus trichocarpa]
 >b|EEE73651.1| predicted protein [Populus trichocarpa]
 Length=609

GENE ID: 7470467 POPTRDRAFT_591844 | hypothetical protein [Populus trichocarpa] (10 or fewer PubMed links)

Score = 292 bits (748), Expect = 8e-77, Method: Compositional matrix adjust.
 Identities = 185/555 (33%), Positives = 301/555 (54%), Gaps = 52/555 (9%)

Query 47	SCETYVTYIAQSPNFLSLTNISNIFDTSPLSIARASNLIEPMDDKLVLKDQVLLPVFTCGCT	106
Sbjct 54	SCQAFLIFKSQ-PSFNSVPISALTSANQEELARINNVTRLSEFPNTNEVI-VPVNCFCF	111
Query 107	GNRSFANISYEINQG-DSFYFVATTSYENLTNWRAVMDLNPVLSPIKLPPIGIQVVFPFLC	165
Sbjct 112	GQYYQANTTIQVTTTRGTYVYVIANETYEGLSTCAALKHLNIHGEYDILLP-GEELQVPLRC	170
Query 166	KCPSKNQLDKEIKYLITYVWKGPDNVSLVSDKFGASPEDIMSENNYQGNFTAANNLPVLI	225
Sbjct 171	CPT+ NQ+ + KYL+ DN+ ++D+F S +DI+ N +N T + + LI	230
Query 226	PVTRLPVLARS-----PS-----DGRKGIRLPVIIIGISLGCTLLVLVLA VLLVV	271
Sbjct 231	PLPTQPTSSQTIIHSNPNISPPSALSPPRNRSKHHYESAGLAAACSLLVISIITAVVFL	290
Query 272	YCLKM--KTLNRSASSAETA-DKLLSGVGSGYVSKPTMYESDADIMEATMNLSSEQCKIGESV	328
Sbjct 291	C K R + + + + + Y + + + + + AT NLS + + I SV	350
Query 329	YKANIEGVKLAVKRFKFEDVTEELKILQKVNHGNLKVLMGVSSNDNGNCFVVYEAENGSL	388
Sbjct 351	Y+ G++LAVK+ DVT+E+ IL++NH NL+KL GV +N G ++V EY ENGSL	409
Query 389	DEWLFSKSCSDTSNSRASLTWCQRISMAVDVAMGLQYMHEAHAYPRIVHRDITSSNILLG	448
Sbjct 410	EWL K +T N W QRI +A+DVA GL Y+H P VH+DI SSN+LL+	463
REWLSCKKFEETGN-----WAQRIQIALDVANGLYLYLHSFTEPAYVHKDIKSSNVLLNG		
Query 449	NFKAKIANFSMARTFTNPMM-----PKIDVFAFGVVLIELLTG	486
Sbjct 464	N+A KIANFS+AR T+ M PKIDV+AFGV+L+EL+TG	523
Query 487	RKAMTTKENGEVVMLWKDIWKFIDQEEENREERLKKWMDPKLESYYPIDYALSLASLAVNC	546
Sbjct 524	+ A+ T ++G +L +I+ I + +N E L ++DP Lt + +AL LA ++V C	581
KDAVFT-QDGREALLSTEIFSIMEN-KNPEVELDDFFVDPALKGSCGTNFALCIAKVSVAC		
Query 547	TADKSLSRPTIAEIV 561	
Sbjct 582	LMKEPARRPSMEEVV 596	

>ref|XP_001783589.1| predicted protein [Physcomitrella patens subsp. patens]
 >b|EDQ51621.1| predicted protein [Physcomitrella patens subsp. patens]
 Length=637

GENE ID: 5946784 PHYPADRAFT_152558 | hypothetical protein [Physcomitrella patens subsp. patens] (10 or fewer PubMed links)

Score = 291 bits (744), Expect = 2e-76, Method: Compositional matrix adjust.
 Identities = 194/611 (31%), Positives = 312/611 (51%), Gaps = 73/611 (11%)

Query 27	VAQSQQDNRTNFSC-PSDSPSCETYVTYIAQSPNFLSLTNISNIFDTSPLSIARAS--N	83
Sbjct 1	+AQ ++ + +C + S SC T+ Y SL + + F+ + +A S N	59
MAQQNQNYNDTEGYACNAAPSSTCSTFAYRTFQAG-ESLRKVGDYFNKTAAAVANVSGMN		
Query 84	LEPMDDDKLVLQVLLPVTCGCTGNRSFANISYEINQGDSFYFVATTSYENLTNWRAVMD	143
Sbjct 60	L L + Q L VP+ C C RS +S+ I +GD+F+ ++ T Y LT ++A+M	119
LLSTTASLKQTQALYVPLDCRCLNARSQMVSHTIVKGDTFWLTSVTEYGGLTRYQAMMA		
Query 144	LNPVLSPIKLPPIGIQVVFPLFCKCPSKNQLDKEIKYLITYVWKGPDNVSLVSDKFGASPE	203
Sbjct 120	NP L IG + P+FC CP+ Q+ YLT+ P + . ++S +FG S	179
SNPSKDGVVNLTIGDTITVPIFCACPTAAQVANGTNYLVTTTVYPSETLDIISARFGISTT		
Query 204	DIMSENNYQGNFTAANNLPVLIPTVRLPVALAR-----SPSDG	240
Sbjct 180	D+ NN + N +L+P+ LP LA +P+	239
DLSRANNVNSSSSILDVNNTLLVPLATPLPLATMDWAPVTSQPSSPATVASPNAAPAVI		
Query 241	RKGGLRPLVIIIGSLGCTLLVLVLA VLLVYVYCLMKMTLNRSASSAETADK-----LL	293
Sbjct 240	K+ P+ IGI+G L L +L ++ + + E + LL	299
TKSASQTPLYAVGAGLTLAAVFAVLLFKASRNSTGPDKPLTEEMKRPNMVHELL		
Query 294	SGVSGYVS--KPTMYETDAIMEATMNLSEQCKIGESVVKANIEGVKLAVKRFKEDVTEEL	351
Sbjct 300	+G+S V KP + + I AT S + I SVYK I G++A+K+ K ++T+EL	359
AGMSDMVGSEKPLVLSHEEIQSATQGFSPENFIQGSVYKGCINGQLVAIKQMGKGNMTQEL		
Query 352	KILQKVNHGNLKVLMGVSSNDNGNCFVVYEEAENGSLDEWLFSKSC---SDTSNSRASLT	408
Sbjct 360	KIL +V+H NLVKL+G+ N ++VYEYA++GSL++ L +++ + S S A L	419
KILCQVHHSNLVKLGLCVGGSENLYLVYEYAKHGSLNDCLRNQAAIGRTTFQSAAYLP		
Query 409	WCQRISMAVDVAMGLQYMHEAHAYPRIVHRDITSSNILLDSNFAKIANFSMARTFTNP--	466
Sbjct 420	WC SRVIALDVASLEYIHNTNPSFVHKDVKTSNILLDENFRAKVANFGMAKSAASADA	479
MMP-----KIDVFAFGVVLIELLTGRKAMTTKENGEVVMLW		
Query 467	M P K DV+AFGVV+E+L+G++A+ E E	502
Sbjct 480	GPLLTRHITGTQGYMAPEYLEHGLVTVKADYVAFGVVVLEILSGKEAVRPEKDEEEQGV	539
Query 503	KD-----IWKIFDQ--EENREERLKKWMDPKLESYYPIDYALSLASLAVNCTADKSLR	554
Sbjct 540	K+ I + + E + E+L+K++DP+L S YPI+ A S+ASIA+ C R	599
KERALSDTIVDVNLNAGTQELTQLRKFIDPQLHSAYPIEIASSIASLAMTCIDPDPAVR		
Query 555	PTIAEIVLSSL 565	
Sbjct 600	PSMKDVTFA LS 610	

>**dbj|BAI79277.1|** LysM type receptor kinase [Lotus japonicus]
dbj|BAI79287.1| LysM type receptor kinase [Lotus japonicus]
Length=667
Score = 286 bits (733), Expect = 4e-75, Method: Compositional matrix adjust.
Identities = 173/591 (29%), Positives = 309/591 (52%), Gaps = 76/591 (12%)

Query 43 DSPPSCETYVTYIAQSPNFLSLTNISNIFDTPLSLSIARASNLEPMDDKLVQDQVLLVPVT 102
+S SC++Y+T+ + SP + + IS + + + P + A++N+ + ++ D ++ VPVT
Sbjct 57 NSVTSCQSILTFKSSPEYNTPSSISYLNSTPSLVAKSNNITDVT+PIITDTMVTVPVT 115
Query 103 CGCTGNRSFANISYEINQ-GDSFSYFVATTSYENLTNWRAVMDLNPVLSPNKLPIGQVVF 161
C C+G R N +Y + G+++ +A +Y+LT +A+M NP + N L G +
Sbjct 116 CSCSGGRYQHNATYLNKKTGETYFSIANNTYQSLTTCQALMAQNPYDAKN-LFAGDDLHV 174
Query 162 PLFKCKPSKNQLDKEIKYLITYWWKPGDNVSLSVSDKFGASPEDIMSENYYGQNFATAANL 221
PL C CP+K D KLY+TY+ G++ +++ FG + ++ N
Sbjct 175 PLRACACPTKKQSDAGFKYLLTLYVSQGESPDSTAEIFGVDTQSVLDANEELDKSVVFYFT 234
Query 222 PVLIPVTRLP-----VLARSPSDGRKGIGIRLPVIIGISLGCTLLVVLAVLL 268
P+L+P+ P + + + VI+G+++G + ++V LL
Sbjct 235 PLLVPLKTEPPARLQIAASPPESPPPAPAGNDSSSSKKWVIVGVGTVGAVCLVV--ALL 292
Query 269 VVYVYCL-----KMKTINRSASSAETADKLLSGVSGYVSKPTMYE 307
V+ C +K ++ + + E+ GV + T Y+
Sbjct 293 VFVFLCFYNRRRRQPAAPPVSVKDFPDSAVKVMVSETTPTESWSLSSEGVRVYAIESTAYK 352
Query 308 TDAIMEATMNLSEQCKIGESVYKANIEGKVLAVKRFKEDVTEELKILQKVNHGNLVKLMG 367
I AT SE+ KI SVY+A+ +G AVK DV+ E+ +L++NH N++L G
Sbjct 353 FGDIGTATKFFSEENKIKGSVYRASFKGDDAAVILNGDVSAINLLKRINHANIIRLSG 412
Query 368 VSSDNDGNCFVVVEYAEANGSLDEWLFSKSCSDTSNSRASLTWCQRISMAVDVAMGLQYMH 427
+ GN ++VYE+AEN SLD+W S+ SL+W QR+ +A DVA L Y+H
Sbjct 413 FCV-HKGNTYLVYFAENDSLDDWLHSEKKYQNS--VSLSWMQRVQIAYDVADALNYLH 468
Query 428 EHAYPRIVHRDITSSNILLDSNFKAKIANFSMARTFTNP----- 466
+ P ++H++ S N+LL+ +AK++NF +AR +
Sbjct 469 NYTNPVLIHKNLKSGNVNLNGKFRAKVSNFGLARAMEDQGEDGGGFQMTRHVVGQTQGYMP 528
Query 467 -----MMPKIDVFAFGVVLIELLTGRKAMTTKEN---GEVVMLWKDIWKFQDQE-EN 514
+ PK+DV+AFGVV++ELL+G+A + GE ++L + + + + + +N
Sbjct 529 PEYTENGLITPKMDVYAFGVVMLELLSGKEATGNGDKNGLGEKMLSETVNHVLEGDNDN 588
Query 515 REERLKKWMDPKLESYIDYALSLASLAVNCTADKSLSRPTIAEIIVLSSL 565
++L+ +MD L Y+D A S+A + A C A SRP I+E+ ++LS
Sbjct 589 VRDKLRLGFMDQTLRDEYPLDLAYSMAEIAKRCVAHDLNRSRPNISEVFMTLS 639

>**ref|XP_002510756.1|** kinase, putative [Ricinus communis]
gb|EEF52943.1| kinase, putative [Ricinus communis]
Length=634

GENE ID: 8269969 RCOM_1602540 | kinase, putative [Ricinus communis]
Score = 283 bits (724), Expect = 5e-74, Method: Compositional matrix adjust.
Identities = 182/572 (31%), Positives = 289/572 (50%), Gaps = 74/572 (12%)
Query 47 SCETYVTYIAQSPNFLSLTNISNIF---DTSPLSIARASNLEPMDDKLVQDQVLLVPTC 103
SC++Y+T+ + P + + IS +F D++ L IA +N+ + L +PV C
Sbjct 56 SCQSILTFRSAPPYTTPTVTSYFLQSDASIL-IASLNNISSDVSSIPPQSQLFIPVNC 114
Query 104 GCTGNRSFA-NISYEINQGDSFYF-VATTSYENLTNWRAVMDLNPVLSPNKLPIGQVVF 161
C G ++ N SY + YF VA +Y+ L+ +A+M NP N L +G++
Sbjct 115 SCFGQFYQHNASYTFLKFSSETYFSVANDTYQGLSTCQALMSQNPYGDRN-LSVGMRLQV 173
Query 162 PLFKCKPSKNQLDKEIKYLITYWWKPGDNVSLSVSDKFGASPEDIMSENYYGQNFATAANL 221
PL C CP+ NQ +YL+TY+ GD +S + + FG P+ I+ N
Sbjct 174 PLRACACPTSNQTAFLGFRYLLTYMVTWGDTISSIONELFGVRPQSIILDANQLSSTSIIIFPFT 233
Query 222 PVLIPVTRLPVLR-----SPSDGRKGIGIRLPVIIGISLGCTLLVVLAVLL 268
P+L+P+T P + + +P G R +G+ LG LL++
Sbjct 234 PILVPLTTPPTTIKASPPPPVSPPPPITPVLPSSGRKWTYVGVLGAALLLIFAVSGF 293
Query 269 VVYVYCL-----CLMKTL-----NRSASSAETADKLLSGVSGYVSKPTMYETDAIMEAT 315
++ Y K+ T+ + SA + ++ G + T+Y+ + AT
Sbjct 294 LFWYPKSKSRKLTTVPIPSSKALQSDSSAVPPDSSTPWRSRSAYGVIESLTLYKFHDQLLAT 353
Query 316 MNLSEQCKIGESVYKANIEGKVLAVKRFKEDVTEELKILQKVNHGNLVKLMGVSSDNIGN 375
SE+ +I SVY + G AVK K DV+ E+ IL+K+NH N++L GV D N
Sbjct 354 DYFSEKNRIKGSVYKGSFKGDAAVKVMKGDSSEISILKKINHSNIIRLSGVCL-YDAN 412
Query 376 CFVYVYEAENGSLDEWLFSKSCSDTSNSRASLTWCQRISMAVDVAMGLQYMHHEAYPRIV 435
++VYE+AENGSL E + +LTW QR+ +A DVA L Y+H + P +
Sbjct 413 TYLVEFAENGSLAE-----NVQTLTWKQRVQIAHDVADALNYLHNNTNPPYI 460
Query 436 HRDITSSNILLDSNFKAKIANFSMARTFTNP-----MM 468
H++ +SNILLD+N +AKIANF+ART N +
Sbjct 461 HKNLKTSNILLDANMRAKIANFGLARTLQNEAEGGLHLTRHVVGQTQGYMAPEYMENGVIT 520
Query 469 PKIDVFAFGVVLIELLTGRKAMTTKENGEVVMLWKDIWKFQDQEENREERLKKWMDPKLE 528
PK+DVFAFGVV++ELL+G+A T +N ML I ++ +N +L +MDP L
Sbjct 521 PKLDVFAFGVILELLSGKEAATYDKNAREEMLSASICRVL-EGDNVRHKLCGFMDPSLG 579
Query 529 SYYPIDYALSLASLAVNCTADKSLSRPTIAEI 560
Y+D A SIA LA C + +RP+ + +
Sbjct 580 KQYPLDLAFLSLAQQLAQTCISHDINARPSVSQV 611

>**ref|XP_002522569.1|** BRASSINOSTEROID INSENSITIVE 1-associated receptor kinase 1 precursor, putative [Ricinus communis]
gb|EEF39869.1| BRASSINOSTEROID INSENSITIVE 1-associated receptor kinase 1 precursor, putative [Ricinus communis]
Length=624

Gene ID: 8259229 RCOM_1014860 | BRASSINOSTEROID INSENSITIVE 1-associated receptor kinase 1 precursor, putative [Ricinus communis]

Score = 280 bits (717), Expect = 3e-73, Method: Compositional matrix adjust.
 Identities = 179/568 (31%), Positives = 303/568 (53%), Gaps = 56/568 (9%)

Query 47	SCETYVTYIAQSPNFLSLTNISNIFDTPLS--IARASNLEPMDDKLVLDQVLLPVTG	104
	SC++Y+T+ A P + S I + + + IA +N+ + ++ ++ +PV C	
Sbjct 56	SCQSYITFRANP-YNSPAKIGYLGSQSEATLIASMNNISCDVATIPTNKQVVVPVNCS	114
Query 105	CTGNRSFA-NISYII-NQGDSFYFVATTSYENLTNWRAVMDLNPLSPNKLPIGIQVVFP	162
	C + N +Y I ++ ++++ +A +Y+ LT +++ + NP N+L G + P	
Sbjct 115	CHAGLYYQHNAATYRIKDENENYFTLANDTYQGLTCQSLWEQNP-YDLINEYAGSDLHVP	173
Query 163	LFCCKPSKNQLDKEIKYLITYVWPKGDNVSLVSDKFGASPEDIMSENNGQNETTAANNLP	222
	L C CP+ NQ +K ++TY+ GD +SL+++ F A+ + ++ N ++ P	
Sbjct 174	LRCACPTPNQTAGSVVKCMLTYMVTWGDYISLIAELFNANEQSVDANELLEDDLIYPFTP	233
Query 223	VLIPIVTRLP---VLARSPSDGRKGIRL-PV-----IIGISLGCTLLVLV-LAV	266
	+L+P+ P + SP R + + PV G +G LLLV +	
Sbjct 234	ILVPLLSEPVSTVDPGYSPPPTRTPVTESSNSKKWVFFGTGIGAVLLVLVAFSA	293
Query 267	LLVYVCLKMTLNRSASSAETADKLLS--GVSGYVSKPTMYETDAIMEATMNLSEQCKI	324
	+ C + ++ ++ +T +S G+ ++ +Y+ D+I AT N SE ++	
Sbjct 294	FSFWYFCRRPSQKSQEPEPATKTDPSVSHVGIEFFIESLIIYKFDSIQTATGNFSEDNRV	353
Query 325	GESVYKANIEGKVLAJKRKFEDVTEELKILQKVNHGNLVLKLMGVSSNDGNCFVYAYAE	384
	SYVK EG AVK DV+ E+ IL+K+NH N+V+L G ++GN ++VY+YAE	
Sbjct 354	KGSVYKGIFEGDHAAVKAMRGDVSSIEIDILKMMNHSNIVRLSGFCV-HEGNTYLVYQYAE	412
Query 385	NGSLDEWLFSKSCSDTSNSRASLTWCQRISMAVDVAMGLQYMEHAYPRIVHRDITSSNI	444
	NGSLDDWLHLYKNDPVS--SSLSWKQRLQIAYNADAFTYLNHYTTPPFVHNRLTTTSNI	469
Sbjct 413		
Query 445	LLDSNFKAKIANFSMARTFTNP-----MMPKIDVVFAG	477
	LL NF+A I NF +AR +N + PK+DVFA+G	
Sbjct 470	LLHGNFRAMITNFGLARKLNSNDQGAPQLTRHVVGTNGYMAPEYLENLITPKLDFVAYG	529
Query 478	VVILIELLTGRKAMTTKENGEVVMLWVKDIWKIFDQEEENREERLKKWMDPKLESYYPIDYAL	537
	VV++ELL+G+KA+ ++ NGE ML+ I + +N E+LK ++DP L P+ +A	
Sbjct 530	VVILELLSGKKAVMSETNGEKMLFALINNNVL-EGDNVREKLIKAFIDPCLRGNIPLHF	588
Query 538	SLASLAVNCTADKSLSRPTIAEVLSLS 565	
	S+A LA +C A RP++ E+ +SLS	
Sbjct 589	SIAQI AKDCVAHDPNDRPSMLEVMSLS 616	

>ref|XP_002990805.1| hypothetical protein SELMODRAFT_11326 [Selaginella moellendorffii]
 >gb|EFJ08078.1| hypothetical protein SELMODRAFT_11326 [Selaginella moellendorffii]
 Length=539

Gene ID: 9659107 SELMODRAFT_11326 | hypothetical protein
 [Selaginella moellendorffii]

Score = 280 bits (717), Expect = 3e-73, Method: Compositional matrix adjust.
 Identities = 190/552 (34%), Positives = 295/552 (53%), Gaps = 31/552 (5%)

Query 38	FSCPSDSPSCETYVTYIAQSPNFLSLTNISNIFDTPLSIIARASNLEPMDDKLVLDQVL	97
	+SC S+S SC+ Y Y A + +L ++ F S +A AS + LV DQVL	
Sbjct 1	YSCVSNST-SCQAYAYRALQGD-TLQSVGLFRRLSVEQLAESQI-AQSATLVPDQVL	56
Query 98	LVPVTCGCTGNRSFANISYEINQGDSFYFVATTSYENLTNWRAVMDLNPLSPNKLPIGI	157
	L+P+ C C RS N +Y I GD+ Y V+ ++ LT ++AV NP+ P L G	
Sbjct 57	LIPLNCSASCGRSQFNATYIIQSGDTLYLVSNQTFQGLTTYQAVERANPLAVPTNLQPGD	116
Query 158	QVVFPLFCPSKNQLDKEIKYLITYVWPKGDNVSLVSDKFGASPEDIMSENNGQNFTA	217
	+VFP+ C CPS Q+ +L+TY PG+ ++ + S +S+N + T	
Sbjct 117	SIVFPIRCACPSSAQVAAGVTSILTVYSIWPGEILDGIARAWNSRTRLASDNTVSGSATL	176
Query 218	ANNLPLVLIPTVTRLPVLARSPSDGRKGIRLPLVIIIGISLGCTLLVLVIAVLLVYVYCLKMK	277
	+ P + + S + +GI++ C VL++ V LV Y + +	
Sbjct 177	SPAAPPANPPNNSPSPDSSSSGNTGM--YVGIAVACVAAVLVLVVALVIFYRRRSR	234
Query 278	TLNRSASSAETAD----LLSGVGSYV--SKPTMYETDAIMEATMNLSEQCKIGESV	328
	+ ++S AE + + LI+G+ G V +P ++ + + +AT N S I SV	
Sbjct 235	KVTKASSYAEPSEKPSPHAPLAGMHGLVDSERPVVFSYEELCDATNNFSASHLIQGSV	294
Query 329	YKANIEGKVLAJKRKFEDVT-EELKILQKVNHGNLVLKLMGVSSNDGNCFVYEAENG	387
	Y+ + ++A+K K T +ELKIL KV+H NLVKL+G+ S +D F+VYEA+NCS	
Sbjct 295	YRGILRKQLVAIKEKMGTTSQELKILCKVHHNSLNVKLIGICSGDD-KLFLVYEAADNG	353
Query 388	LDEWLFSKSCSDTSNSRASLTWCQRISMAVDVAMGLQYMEHAYPRIVHRDITSSNILL	447
	L SC A+ W R+ +A+DVA GL+Y+H++ P VH+D+ SSNILL	
Sbjct 354	-----SSCLHNRTPAATAIWTRLQVAMDVATGLEYIHDYTKPSFVHKDVKSSNILL	407
Query 448	SNFKAKIANFSMARTFTNP--MMPKIDVFAFGVVLIELLTGRKAMTTKENGEVVMLWKD	505
	+N +AK+ANF MAR + + K+DV+AFGVVL+EL TGR+A+ + G D	
Sbjct 408	ANLRAKAVANFGMALARLYLTHGFVTTKVDVYAFGVVLLFTRGAILSTGTGSEKQYLADA	467
Query 506	W----KIFQEEENRE--ERLKKWMDPKLESYYPIDYALS LASLAVNCTADKSLSRPTIAE	559
	+ F ++N E E+LK W DP L++ P D AL+ +A +C +RP + +	
Sbjct 468	FVKLTDGFAGDDNDEKIEKLKHADPILDNAVWPWDIALNFVEARSCVDADPDARPNMKD	527
Query 560	IVLSSLSSLLTQPS 571	
	+ LS L + S	
Sbjct 528	VTFKLSKLLESS 539	

>ref|XP_002277331.1| PREDICTED: hypothetical protein [Vitis vinifera]
 Length=638

Gene ID: 100258108 LOC100258108 | hypothetical protein LOC100258108
 [Vitis vinifera]

Score = 280 bits (716), Expect = 4e-73, Method: Compositional matrix adjust.

Identities = 188/628 (29%), Positives = 313/628 (49%), Gaps = 94/628 (14%)

Query 17	LVIMLFSTNIVAQSQD-----NRTN-FSCPSDSPSCETVYTYIAQSPNFL +V++L VAO+QQ N TN F C + P SC +Y+T+ + P++	62
Sbjct 1	MVLLLWVISVAQQSYVNHHQLDCDNFNETNGFQC--NGRSCHSYLTFRSAPPYD	58
Query 63	SLTNISNIFDTSPLSIARASNLEPMDDKLVKDQVLLPVTCGCTGNRSFANISYEINQGD S +I+ + ++ P IA + + +D + KD VL+VPV C C+G+ N +Y +	122
Sbjct 59	SPPSIAYLNSEPAQIATINEVSVD-TISKDTVLIVPVNCSCSGDFYQHNNTYTLKSAS	117
Query 123	SFYI-VATTSYENLTNWRAVMIDLNPVLSPKNLPIGIQVVFPLCKCPSKNQLDKEIKYLI YF +A +Y+ LT +A+ NP N L +G+ + PL C CP+ NQ YL+	181
Sbjct 118	ETYFSLANNTYQGLTTQCALKAQNPYDYRN-LSVGLHLQVPLMCAPTAAGFNYLL	176
Query 182	TYWKPGDNVSLVSDKFGASP-EDIMSENNYQGQFTAANNLPVLIPVTRLVPLARS--- +Y+ GD + ++ FG + I N P+P+ P ++	236
Sbjct 177	SYLTVWGDITDSIAKIFGVDDVQSIYDANRLSSTSIVYQPFPTILVPLKNPPSKIQTTVSS	236
Query 237	-----PSDGRKGIGRLPVIIGISLGCTLLVLVLAVLLVYVYCLKMKT----- PS G + V IG +G LLVL++ ++ + + +	278
Sbjct 237	PPAPSPETPMVPSGGGSNSKKWWFIGAGIGAALLVLLISSGMMFCFFRRRQSGQDKPV	296
Query 279	-----LNRSASSAAETADKLLSGVSGVSKPTMYETDAIMEATMLNSEQCKIGESVYK L+S + + L G+ + T+Y+ + + FA E + I SYV+	330
Sbjct 297	LDLGEATKLKSLENKTSMSISLEGIRIEMESITVYKYEELQKAAGYFGEANRIKGSVYR	356
Query 331	ANIEGKVLAVKRKFEDVTEELKILQKVNHGNLVLMGVSSNDGNCVVFVYEAENGSLDE A+ +G A+K K DV+EE+ IL+++NH +++L G + GN ++VYEAENG+L +	390
Sbjct 357	ASFKGDDAAIKMMKGDVSEEINLKQINHNSKVIRLSGFCI-HAGNTYLVYEAENGALRD	415
Query 391	WLFS--KSCSDTSNSRASLTWCQRISMAVDVAMGLQYMHEAYPRIVHRDITSSNILLDS WL ++CS + + L W QR+ +A D A L Y+H P +H+++ SNIILD	448
Sbjct 416	WLHGMDGETCS-----TLGWKQRVQIAYDAADALNLYLHNHFISPPCIHKNLKISNILLDG	468
Query 449	NFKAKIANFSMARTFTNP-----MMPKIDVFAFGVV N + K+ NF +AR N + PK+D+FAFGVV	479
Sbjct 469	NMRGVKVTNFGLARRLGNEEGDGGGLQLTRHVVGTQGYMAPEYVENGVVTPKLDIFAFGVV	528
Query 480	LIELLTGTRKRAMTT--KENGEVVMLWKDIWKFIDQEEENREERLKWMDPKLESYPIDYAL ++ELLTG+A + KE GE++ + I ++ Q+N ++L+ ++DP L YP D A	537
Sbjct 529	IILELLTGKEAAPSQKKEGELLSV--SINEVL-QGDNVRDKLRFIDPCLAHEYPDFLAF	585
Query 538	SLASLAVNCTADKSLSRPTIAEIVLSSL 565	
Sbjct 586	SMQAQIAKSCVAHDLNARPMTSDIFVILS 613	

>**ref|XP_002974494.1|** hypothetical protein SELMODRAFT_11327 [Selaginella moellendorffii]
gb|EFJ24716.1| hypothetical protein SELMODRAFT_11327 [Selaginella moellendorffii]
Length=539

Gene ID: 9657733 SELMODRAFT_11327 | hypothetical protein
[Selaginella moellendorffii]

Score = 279 bits (714), Expect = 7e-73, Method: Compositional matrix adjust.
Identities = 189/552 (34%), Positives = 294/552 (53%), Gaps = 31/552 (5%)

Query 38	FSCPSDSPSCETVYTYIAQSPNFLSLTNISNIFDTSPLSIARASNLEPMDDKLVKDQVL +SC S+S SC + Y A + +L ++ F S +A AS + LV DQVL	97
Sbjct 1	YSCVSNST-SCQAYAAYRALQGD--TLQSVGLRFLSVEQLAEASQI-AQSATLVPDQVL	56
Query 98	LPVPTCGCTGNRSFANISYEINQGDSFYFVATTSYENLTNWRAVMIDLNPVLSPKNLPIGI L+P+ C C RS N +Y A + GD+ Y V+ ++ LT ++AV NP+ P L G	157
Sbjct 57	LIPPLNCSCASGRSOFNATYIIQSGDTLYLVSNGTFOGLLTYYQAVERANPLAVPTNLQPGD	116
Query 158	QVVFPLFCKPCKPSKNQLDKEIKYLITYVWKPGDNVSLVSDKFGASPEDIMSENNYQGQFTA +VFP+ C CPS Q+ + L+TY PG+ + ++ + S + S+N + T	217
Sbjct 117	SIVFPIRCACPSSAQVAAGVTSIVPGEILDGIARAWNVSRTRIASDNTVSGSATL	176
Query 218	ANNLPLVLPVTRPLVLRSPDRGKGGIPLVIIIGISLGCTLLVLVLAVLLVYVYCLKMK + P + S + S + + GI++ C VL++ + LV Y + +	277
Sbjct 177	SPAAPPANNPPNNSPSPDSSSSGSNTGM--YVGIAVACVAALLVVLALVIFYRRRPR	234
Query 278	TLNRSASSAAETADK-----LLSGVSGYV--SKPTMYETDAIMEATMLNSEQCKIGESV + ++S AE + + LL+G+ G V + P ++ + + +AT N S I SV	328
Sbjct 235	KVTKASSYAEPSPKQPSPHAPLAGMHGLVDSERPVVFYSYEELCDATNNFSASHLIQGSV	294
Query 329	YKANIEGKVLAVKRKFEDT-EELKILQKVNHGNLVLMGVSSNDGNCVVFVYEAENG Y+ + ++A+K K T +ELKIL KV+H NLVKL+G+ S +D F+VYEA+NGS	387
Sbjct 295	YRGILRKQLVAIKEKMGGTTSQELKILCKVHHNSNLVKLIGICSGDD-KLFLVYEAADNGS	353
Query 388	LDEWLFSKSCSDTSNSRASLTWCQRISMAVDVAMGLQYMHEAYPRIVHRDITSSNILL L SC A+ W R+ +A+DVA GL+Y+H++ P VH+D+ SNIILLD	447
Sbjct 354	-----SSCLHNRTPAATAIWNTRLQVAMDVATGLEYIHDTYKPSFVHKDVKSSNILLD	407
Query 448	SNFKAKIANFSMARTFTNP--MMPKIDVFAFGVV +N +AK+ANF MAR + + K+DV+AFGVVL+EL TGR+A+ + G D	505
Sbjct 408	ANLRAKVANFGMARLYLTHGFVTKVWDYAAFVVLLFTRGAREILSTGTGSEKQYLADA	467
Query 506	W----KIFDQEENRE--ERLKKWMDPKLESYYPIDYALSASLAVNCTADKSLSRPTIAE + F + +N E E+LK W DP L++ P D AL+ +A +C +RP +	559
Sbjct 468	FVKLTDGFAGDDNDEKIEKLKHADPILDNAWPWDIALNFVEVARSCVDADPDARPNKD	527
Query 560	IVLSSLSSLTQPS 571	
Sbjct 528	+ LS L + S VTFKLSKLESS 539	

>**emb|CBI17583.3|** unnamed protein product [Vitis vinifera]
Length=1305

Sort alignments for this subject sequence by:
E value Score Percent identity
Query start position Subject start position

Score = 277 bits (709), Expect = 3e-72, Method: Compositional matrix adjust.
Identities = 171/565 (30%), Positives = 298/565 (52%), Gaps = 56/565 (9%)

Query 47 SCETYVTYIAQSPNFLSLTNISNIFDTSPLSIARASNLEPMDDKLVQDQVLLVPVTCGCT 106
 +C+TY+ + ++SP + ++++IS++ + P +A+ +++ +V+ VPV C C+
 Sbjct 719 TCQTYLIFRSESP-YNNVSSISDLSQSQLAQINSVTETATFDTNKEVI-VPVNCSCS 776

Query 107 GNRSFANISYEINQGDSFYFVATTSYENLTNWRAVMDLNVLSPNKLPIGIQVVFPFLCK 166
 GN S N SY + GD +A +++ L+ +A+++ NP +S L G + PL C
 Sbjct 777 GNYSQNTNTSYVVVKNGDYPLWIANNTFQGLSTCQALLNQNQPSVSATNLNPGBTITVPLRCA 836

Query 167 CPSKNQLDKEIKYLITYWKPGDNVSLVSDKFGASPEDIMSENNGQNFATAANLPVLIP 226
 CP+K Q D +KYL++Y+ GD VS +S +FG E + N + T +LIP
 Sbjct 837 CPTKAQSDAGVKYLMSYLVAYGDTVAISGRFVGVDTERTLEANELSEQDTINPFTILLIP 896

Query 227 VTRLPVLARSPSDGRKGIRLPIIGISLGCTLLVVLAVLVLVYV-YCLKMKTLNRSASS 285
 + P +++ I+ V + + + ++L+ +++V + K K N +
 Sbjct 897 LQNPPSSQT-----IKTWVYVIVGVAAGVVLFFGYVIFVKFFRKTKKKNDQIAV 948

Query 286 AET-----ADKLLSGVSGYVSKPTMYETDAIMEATMNLSEQCKIGESVYKANIE 334
 +E+ + + +S + + + AT N S C I SVY+ I+
 Sbjct 949 SESFKPKEPLKPLKVEEHEFFESISSMAQSVKVYKFEELQSATDNFSPSPCLIKGSVYRGTIK 1008

Query 335 GKVLAVKRFKEDVTEELKILQKVNHGNLVLKGVSSNDGNCFVYVYEAENGSLDEWLFS 394
 G + A+K+ +V+ E+ +L K+NH N++L G+ NDG+ +V+EYA NGSL +W+
 Sbjct 1009 GDLAIAKKMDGNVSNEIALLSKINHFNVIRLSGICF-NDGHWYLVHEYAVNGSLSDWIYY 1067

Query 395 KSCSDTSNSRASLTWCQRISMADVAMGLQYMHEAYPRIVHRDITSSNILLDSNFKAKI 454
 + N R L W QRI +A+DVA GL Y+H H P +H+D+ S+N+LLD +E+AKI
 Sbjct 1068 NN-----NDRFLVWTQRIQIALDVATGLNLYLHIVSPSYIHKDMKSNVLLDGFRAKI 1122

Query 455 ANFSMARTFTNP-----MMP-----KIDVFAFGVVLIELLTGRK 488
 ANF AR+ M P K+DV+AFCV++E+ TG K
 Sbjct 1123 ANFDQARSAAEGQCGQFALTRHIVGTYGMAPEYLENGLISTKLVDVYAFGVIMLEIFTG-K 1181

Query 489 AMTTKENGEVVMLWWDKIWKIFDQEENREERLKKWMDPKLESYYPIDYALSLASLAVNCTA 548
 + GE + L + + + E++ +E+L ++DP L+ YP + A+ + L +C
 Sbjct 1182 EVAALYGGESIHLSEVLAABL-HEDDGKEKLQDFIDPSLDGNYPPELAIFMIRLIDSCLT 1240

Query 549 DKSLSRPTIAEIVLSSLTLTQPSPA 573
 RP + EIV SLS + S A
 Sbjct 1241 KAPAGRDPDMDEVQSLSRILASSQA 1265

Score = 273 bits (698), Expect = 6e-71, Method: Compositional matrix adjust.
 Identities = 177/557 (31%), Positives = 297/557 (53%), Gaps = 56/557 (10%)

Query 47 SCETYVTYIAQSPNFLSLTNISNIFDTSPLSIARASNLEPMDDKLVQDQVLLVPVTCGCT 106
 Sct + + + P + ++++IS++ + P +A+ +++ +V+ VPV C C+
 Sbjct 74 SCQAFLIFRSEPP-YNDVSSISDLSQSQLAQINSVDETATFETKKEVI-VPVNCSCS 131

Query 107 GNRSFANISYEINQGDSFYFVATTSYENLTNWRAVMDLNVLSPNKLPIGIQVVFPFLCK 166
 G S AN SY + GD++ +A +E L+ -A+ L+ N + G ++ PL C
 Sbjct 132 GEFSQANTSYVQHGDTYLLIANTFQGLSTCQALRSQRTSLTN-IYTGTKLTVPLRCA 190

Query 167 CPSKNQLDKEIKYLITYWKPGDNVSLVSDKFGASPEDIMSENNG-QNFTAANLPVL 225
 CP+RNQ D +KYL++Y+ GD VS +S +FG + N QN P +
 Sbjct 191 CPTKNQSDVGVKYLMSYLVASGDIVVSSISVFRGVDTGTMLEANLSEQN-----PNIY 243

Query 226 VTRLPVLARSPSDGRKGIRLPIIGISLGCTLLVVLAVLVLVYVYCLKMKTLNRSAS 284
 P T L + L PS + +V+G+ G L++L +V+ + + K + A
 Sbjct 244 PFTTLLIPLQNLQPLSSQTIKTWVYVYVAGSALVLLFGSVIFFKFFRKTRKTDPIAI 303

Query 285 S-----AETADKLLSGVSGYVSKPTMYETDAIMEATMNLSEQCKIGESVYKANIE 334
 S E + L +S +Y+ + + AT N S C I SVY+ I+
 Sbjct 304 SESFEACEKPLKEEKFLESISSIAQSLSKVYKFEELQSATDNFSPNCRIKGSVYRGTIK 363

Query 335 GKVLAVKRFKEDVTEELKILQKVNHGNLVLKGVSSNDGNCFVYVYEAENGSLDEWLFS 394
 G + A+K+ +V+ E+ +L K+NH N++L G+ NDG+ +V+EYA NG L +W++
 Sbjct 364 GDLAIAKKMDGEVSNEIALLNSKINHFNVIRLSGICF-NDGHWYLVHEYAVNGPLTDWIYN 422

Query 395 KSCSDTSNSRASLTWCQRISMADVAMGLQYMHEAYPRIVHRDITSSNILLDSNFKAKI 454
 + +SR L W QRI +A+DVA GL Y+H H P +VH+DI S N+LLDS+F+AKI
 Sbjct 423 ---NNDSDSRF-LVWMQRQIQLDVATGLNLYLHSYTPPYVHDKSGNVLLDSDFRAKI 477

Query 455 ANFSMARTFTNP-----MMP-----KIDVFAFGVVLIELLTGRK 488
 ANF +AR+ M P K+DV+AFCV++E+LTG++
 Sbjct 478 ANFGLARSAAEGQEGQFALTRHIVGTYGMAPEYLENGLVSTKLVDVYAFGVIMLEMTGKE 537

Query 489 AMTTKENGEVVMLWWDKIWKIFDQEENREERLKKWMDPKLESYYPIDYALSLASLAVNCTA 548
 E GE + L D+ E + +E+L ++DP L YP++ A+ + L +C
 Sbjct 538 VAALYE-GENMHL-PDVLVAVLHEGDGEKLRNFIDPSLSGNYPLELAIVMIRLIDSCLK 595

Query 549 DKSLSRPTIAEIVLSSL 565
 SRP + EIV +LS
 Sbjct 596 KSPASRPDMDEVQSLSRILASSQA 612

>**ref|XP_002510333.1|** serine-threonine protein kinase, plant-type, putative [Ricinus communis]

gb|EEF52520.1| serine-threonine protein kinase, plant-type, putative [Ricinus communis]
 Length=637

Gene ID: 8260932 RCOM_1593420 | serine-threonine protein kinase, plant-type, putative [Ricinus communis]

Score = 276 bits (707), Expect = 5e-72, Method: Compositional matrix adjust.
 Identities = 168/555 (30%), Positives = 295/555 (53%), Gaps = 49/555 (8%)

Query 47 SCETYVTYIAQSPNFLSLTNISNIFDTSPLSIARASNLEPMDDKLVQDQVLLVPVTCGCT 106
 +C+ ++ + ++ P + S IS + S +AB+ N+ + + + +V+ VPV+C C
 Sbjct 54 TCQAFLIFRSPR-YDASPTISALTSAQEEARFNNVTGLSEFPLNKEVI-VPVSCSCL 111

Query 107 GNRSFANISYEINQGDSFYFVATTSYENLTNWRAVMDLNVLSPNKLPIGIQVVFPFLCK 166
 G AN S+++ S++ +A+ +YE L+ ++ N + L +G ++ PL C
 Sbjct 112 GQYYQANTSFQVASDHYSFTIASQTYEGLSTCASLKKAN-IYGEFDLALGAEIQVPLRCA 170

Query 167 CPSKNQLDKEIKYLITYWKPGDNVSLVSDKFGASPEDIMSENNGQNFATAANLPVLIP 226

Sbjct	171	CP+ +Q+ E KYL+T+ D+++ ++++F S E I+ N ++ T + +LIP SCTASQVRNETKYLLTFPISESDHIAAERFNVSKESEIIDANGLRESPTIYPTDTILIP	230
Query	227	VTRLPVLAR-----SPSDGRKGIRLPIVIIIGISLGCCTLLVILVLAVALVLYV +T P ++ SP D R+ +L +GI+ C+LLVL + V++++	271
Sbjct	231	LTEPSNSQTIIHENPTEVPPLASPPDNRSRKRKLYEVGITAACSLVLSIIVVILFL	290
Query	272	YCLKMKTNRASSAETADKLLSGVSGYVSKPTMYETDAIMEATMNILSEQCKIGESVYKA + + + L ++ ++ + + + +AT N S + I S+Y	331
Sbjct	291	LRKDRRHKFPEINRRREQEDLRLIEIASVEQVLKVFGLEEVKKATDNFSSKHIIKGSLYWG	350
Query	332	NIEGVKLAVKRFKEDVTEELKILQKVNHNGLVLMGVSSDNDNCFCVVYEAYENGSLDEW G++LA+K+ DV++E+ IL++NH NL+KL GV +N G ++ +EY +NGSL EW	391
Sbjct	351	EFNGQILA1KKMNRDVSKEVNIIKLRINHFNLIKLGVC-ENIGCFYLFFEYMKNGSLQEW	409
Query	392	LFSKSCSDTSNSRASLTWCQRISMAVDVAMGLQYMHEAYPVHARDITSSNILLDSNFK + D +W QRI +A+D+A GL Y+H P VH+DITS +ILLD+N +	451
Sbjct	410	LSRERFEDVG-----SWNQRIQIALDIANGLFYLSFTEPACVHKDITSGHILDDNNLR	463
Query	452	AKIANFSMARTFTNPMM-----PKIDVFAGFVVLIELLTGRKA AKIANFS+AR N ++ PKIDV+AFG+VL+EL+TG+ A	489
Sbjct	464	AKIANFSALARAAANAVLTKHIEGTRGYMAPEYYQAGQVTPKIDVYAFIVLLELITGKDA	523
Query	490	MTTKENGEVVMLWDKIFDQEENREERLKKWMDPKLESYYPIDYALSLASLAVNCTAD + ++ G+ +L K I+ + ++ EN E L +DP AL LA +++ C	549
Sbjct	524	VFMRD-GKETLLSKAIFSVMEK-ENAEALAFVIDPSFTGGRQSKLALRARVSLACLTQ	581
Query	550	KSLSRPTIAEIVLVL 564 RP++ E+V +L	
Sbjct	582	VPARRPSMGEVVSTL 596	

>**dbj|BAI79276.1|** LysM type receptor kinase [Lotus japonicus]
Length=633

Score = 276 bits (705), Expect = 7e-72, Method: Compositional matrix adjust.
Identities = 193/612 (31%), Positives = 315/612 (51%), Gaps = 93/612 (15%)

Query	38	FSCPSDSP-PSCTETYVTYIAQSPNFLSITNISNIFDTSPLSIARASNLEPMDDKLVKDQV ++C S +C+ Y+T+ Q P + S+ IS + + +A + ++ + + +	96
Sbjct	49	YTCNGGSANHTCQAYLTFRTO-PIYNSVYTISTLSSDARHLAETMSVS-QNTTFETNKL	106
Query	97	LLPVTCGCTGNRSFANISYEINQGDSFYFVATTSYENLTNRAVMDLNPNVLSPNKLPIG ++PV C C G AN SY D+ + +A ++E LT +A+M N +P L +G	156
Sbjct	107	VIVPVQCSCAGEYYYQANTSYAFQNTDTPFSIANNTFEGLTTCQALMHENH--NPGHLYLG	164
Query	157	IQVFVPLFKCPSKNQLDKEIKYLITYVWKPGDNVSLVSDKF GASPEDIMSENNGQNFT ++ PL C CP+KNQ +K IKYL++Y+ GD+VS++S+KFG S + + N+ + T	216
Sbjct	165	RELTVPVLCACPTKNQTEKGKIKYLLSYLVNWGDSVSVISEKFGVSCNNTLEANSL--SLT	222
Query	217	AANNLP---VLIPVTRLVPLARS-----PSDGRKGIRLPIVIIIGISLG A P +L+P+ P +++ + + + L V++G G	256
Sbjct	223	KAKIYPFTTLLVPLHDKPSNSQTILQSQPSSTSSPPSSSTHQSSNKTWLYVVVG--G	279
Query	257	CTLLVLVLAVLVLVYVY-----CLKMKTNRASSAETADKLLSG-----VSGYVS L+++ AV+ Y L T++ S + + ++ G + G	301
Sbjct	280	VFALIVLTAVIFCIHYHKGRKKDDSLSQLTVSESFENQQLGKEMKKGDGKLSEFIHGIAQ	339
Query	302	KPTMVEATDAMEATMNLSEQCKIGESVYKANIEGVKLAVKRFKEDVTEELKILQKVNHN +Y + I AT NL+ + I SVY+ + G ++A+K+ + DV+E++IL KVNH N	361
Sbjct	340	SFKVYSEEIQRATNNLNSSLIKGSVYRGVMGDLVAIKKTEGDVSKEIQIILNKVNHSN	399
Query	362	LVKLMGVSSDNDGCFVVEYEAENGSLDEWLFSKCSDTDNSRASLTWCQRISMAVDVAM ++L GVS N+G ++VYEYA NG L EW+F L+W QRI +A+DVA+	421
Sbjct	400	VIRLSGVSF-NEGQWYLVYEAANGPLSEWIFFGKF-----LSWTQRIQIALDVAI	449
Query	422	GLQYMHEAYPRIVHARDITSSNILLDSNFKAKIANFSMARTFTNP----- GL Y+H P +H+D+ SSNILLDS+F+AKIAN S+AR+	466
Sbjct	450	GLDYLHSFTSPPHIHKDLSSNILLDSDFRAKIANLSLARSVKGVDDEDDQFLATRNIVGT	509
Query	467	---MMP-----KIDVFAFGVVLIELLTGRK--AMTTKENGEVVMLWWDKIFDQ M P K+DV+AFG+ ++E+LTG++ A+ ++N K++ +	511
Sbjct	510	RGYMAPEYLENGLVSTKLDVYAFGVLMLIEILTGKEVAILAEDNN-----KNLSGVLSA	563
Query	512	EENREERLKKWMDPKLESYYPIDYALSLASLAVNCTADKSLSRPTIAEIVLSSLTQPS EERLK++MDP L+S YP + A+ + + V C SRP++ EIV +LS T S	571
Sbjct	564	VLG-EERLKEMFDPLSQLSNYPFELAMFVFEIIVGCIEKDPAWSRSMQEVPTLS-RTMNS	621
Query	572	PATLERSLTSSG 583 + E S+ SG	
Sbjct	622	SLSWEMSVNISG 633	

>**dbj|BAI79286.1|** LysM type receptor kinase [Lotus japonicus]
Length=633

Score = 276 bits (705), Expect = 8e-72, Method: Compositional matrix adjust.
Identities = 192/612 (31%), Positives = 315/612 (51%), Gaps = 93/612 (15%)

Query	38	FSCPSDSP-PSCTETYVTYIAQSPNFLSITNISNIFDTSPLSIARASNLEPMDDKLVKDQV ++C S +C+ Y+T+ Q P + S+ IS + + +A + ++ + +	96
Sbjct	49	YTCNGGSANHTCQAYLTFRTO-PIYNSVYTISTLSSDARHLAETMSVS-QNTTFETNKL	106
Query	97	LLPVTCGCTGNRSFANISYEINQGDSFYFVATTSYENLTNRAVMDLNPNVLSPNKLPIG ++PV C C G AN SY D+ + +A ++E LT +A+M N +P L +G	156
Sbjct	107	VIVPVQCSCAGEYYYQANTSYAFQNTDTPFSIANNTFEGLTTCQALMHENH--NPGHLYLG	164
Query	157	IQVFVPLFKCPSKNQLDKEIKYLITYVWKPGDNVSLVSDKF GASPEDIMSENNGQNFT ++ PL C CP+KNQ +K IKYL++Y+ GD+VS++S+KFG S + + N+ + T	216
Sbjct	165	RELTVPVLCACPTKNQTEKGKIKYLLSYLVNWGDSVSVISEKFGVSCNNTLEANSL--SLT	222
Query	217	AANNLP---VLIPVTRLVPLARS-----PSDGRKGIRLPIVIIIGISLG A P +L+P+ P +++ + + + L V++G G	256
Sbjct	223	KAKIYPFTTLLVPLHDKPSNSQTILQSQPSSTSSPPSSSTHQSSNKTWLYVVVG--G	279
Query	257	CTLLVLVLAVLVLVYVY-----CLKMKTNRASSAETADKLLSG-----VSGYVS L+++ AV+ Y L T++ S + + ++ G + G	301
Sbjct	280	VFALIVLTAVIFCIHYHKGRKKDDSLSQLTVSESFENQQLGKEMKKGDGKLSEFIHGIAQ	339

Query	302	KPTMYETDAIMEATMNLSEQCKIGESVYKANIEGKVLAVKRKFEDVTEELKILQKVNHGN +Y + I AT NL+ I SVY+ + G ++A+K+ + DV++E++IL KVNH N	361
Sbjct	340	SFKVYSFEEIQRATNNLNSSSLIKGSVYRGVMNGDVLVAIKKTGDSKEIQIILKVNHSN	399
Query	362	LVKLMGVSSNDGCNCFVVVEYAENGSLDEWLFSKSCSDTSNSRASLTWCQRISMADVAM ++L GVS N+G ++VYEYA NG L EW+F L+W QRI +A+DVA+	421
Sbjct	400	VIRLSGVSF-NEGQWYLVYEEAANGPLSEWIFFGKF-----LSWTQRIQIALDVAI	449
Query	422	GLQYMHEHAYPRIVHRDITSSNILLDSNFKA KIANFSMARTFTNP----- GL Y+H P +H+D+ SNNILLDS+F+AKIAN S+STAR+	466
Sbjct	450	GLDYLHSFTSPPHITHKDLSKSNILLDSDFRAKIANLSSLARSKVGDDEDDQFLATRNIVGT	509
Query	467	--MMP-----KIDVFAFGVVLIELLTGRK--AMTTKENGEVVMLWKDIWKFIDQ M P K+DV+AFGV++E+LTG++ A+ ++N K++ +	511
Sbjct	510	RGYMAPEYLENGLVSTKLVDYAFGVMLMLEILTGKEVAAILAEDNN-----KNLSGVLSA	563
Query	512	EENREERLKWMKPLESYYPIDYALSLASLASLAVNCTADKSLSRPTIAEVLSISLLTQPS EERLK++MDP L+S YP +A+ + + V C SRP++ EIV +LS T S	571
Sbjct	564	VLG-EERLKEFMDPLSQLSNSYPFELAMFVFEIIIVGCIEKDPA SRPSMQUEIVPTLS-RTMNS	621
Query	572	PATLERSLTSSG 583 + E S+ SG	
Sbjct	622	SLSWEMSVNISG 633	

>gb|ABQ59612.1| LYK4 [Glycine max]
Length=633

Score = 270 bits (689), Expect = 5e-70, Method: Compositional matrix adjust.
Identities = 191/646 (29%), Positives = 329/646 (50%), Gaps = 90/646 (13%)

Query	4	FFPFLPLHSQIILCLVIMLFSTNIVAQSQQDNRTNFSCP-----SDSPPSCET FFP+P+ I L+I FS + Q +CP + + SC++	50
Sbjct	3	LFPPIPI---IIFTLIHNFSQ-ILGQQPYIGLTVACPRGNKNSIRGYTCNGANHSCQS	59
Query	51	YVTYIAQSPNFLSLTNISNIFDTSPSLSTARASNLEPMDDKLVKDQVLLPVTCGCTGNRS Y+T+ +Q P + S+ IS + + P +A+ +++ M+D ++++++VPV C C G	110
Sbjct	60	YLTFRSQ-PIYNSVKTISTLLGSDPSQLAKINSVS-MNNTFETINKLVIVPVNCSAGEYY	117
Query	111	FANISYEINQGDSFYFVATTSYENLTNWRAVMDLNPVLSPNPKLPIGIQVVFPLFCCKPSK N SYE + + + +A + +E LT +A+ + N +P + G + ++ PL C CP+K	170
Sbjct	118	QTNTSYEFHNSETYFLIANNTFEGLTTCQALEQNQH--NPANIYPGRRLLVPLRCAPTK	175
Query	171	NQLDEIKYLITYVWKPGDNVSLVSDKFGASPEDIMSENNYQGNFTAANNLP---VLIPV NQ +K I+YL++Y+ GD+VS +S+KFG + + N T A P +L+P+	227
Sbjct	176	NQTEKGIRYLLSYLVNWGDSVSFISEKFGVNFMTTLEANTL--TLTQATIYPFTTILVPL	233
Query	228	TRLPVLA RSPSDGRGGI RLPII GISLGCTLL-----VLVLA VLLVYVYCLKMK P + + + S R+ P S T + + + +V L + + + +	277
Sbjct	234	HDKPSSSQTVSPTRTPPPSPSSDHSSNKTVWYVVVGVVGAIALISVLCAVIFFTRYR	293
Query	278	TLNRSASSA-----ETADKLLSGVSGYVSKPMTYETDAIMEATMNLSEQ + S + +KL +SG +Y + + AT N S	321
Sbjct	294	KNRKKDDSVVVGSKSFEAIEEKPEVKVNEKLSEIIISGIAQSFKVYNFEELQRATDNFSPS	353
Query	322	CKIGESVYKANIEGKVLAVKRKFEDVTEELKILQKVNHGNLKVLMGVSSNDQNCFVVYE I SVY+ I G + A+KR + DV+E++IL K+NH N++L GVS ++G ++VYE	381
Sbjct	354	SWIKGSVYRGVINGDLAAIKRIEGDVSKEIEILINKHNSVIRLSGVSF-HEGGWYLVYE	412
Query	382	YAENGSLDEWLFSKSCSDTSNSRASLTWCQRISMADVAMGLQYMHEHAYPRIVHRDITS YA NG L EW++ + + L+W QR+ +A+DVA GL Y+H P +H+DI S	441
Sbjct	413	YAANGDLSEIYFHNVNG----KFLSWTQRMQIALDVATGLDYLHSFTSPPHIHKDINS	467
Query	442	SNILLDSNFKA KIANFSMARTFTNP-----MMP-----KIDVFA SNILLD +F+ K+ N S+STAR M P K+DV+A	475
Sbjct	468	SNILDGDFRGKVNTLSSLARCLEGGDDQLPATRHIVGTRGYMAPEYLENGLVSTKLDVYA	527
Query	476	FGVVLIELLTGRK--AMTTKENGEVVMLWKDIWKFIDQEENREERLKWMKPLESYYPI FGV++E++TG++ A+ T++ ++ + I EE+ +E LK++DP L P+	533
Sbjct	528	FGVLMLEMVTGKEVAAILTEDETKLSHVLSGILG---EESKEMLKEFVDPSPGENCPL	583
Query	534	DYALSLASLAVNCTADKSLSRPTIAEVLSLSLLTQPSPATLERSL 579 + A+ + + NC SRP++ EIV S+S T S + ERS+	
Sbjct	584	ELAMFVIEMIDNCI KTDPSRPSVHEIVQSMS-RTLKSSLWERSM 628	

>emb|CBI40796.3| unnamed protein product [Vitis vinifera]
Length=680

Sort alignments for this subject sequence by: E value Score Percent identity Query start position Subject start position				
Score = 269 bits (687), Expect = 1e-69, Method: Compositional matrix adjust. Identities = 170/518 (32%), Positives = 279/518 (53%), Gaps = 45/518 (8%)				
Query	70	IFDTSPLSIARASNLEPMDDKLVKDQVLLPVTCGCTGNRSFANISYEINQGDSFY-VA + + +P IA + + ++ K+ KD VL+PVV C C+G+ N SY + YF +A	128	
Sbjct	151	LLNSNPSDIATINQISDVN-KIPKDTVLLIVPVNCSCSGHFYQYNASYTLKYDFENYFTLA	209	
Query	129	TTSYENLTNWRAVMDLNPVLSPNPKLPIGIQVVFPLFCKCPSKNQLDKEIKYLITYVWKPG + + LT +A+ NP N L +G+ ++ PL C CP+ NQ YL+TY+ G	188	
Sbjct	210	NNTYQGLTTCQALKAHNPYYYRN-LSVGMDLLVPLMCAPCTANQTAAGFNYLLTYLWTWG	268	
Query	189	DNVSLVSDKFGASPEDIMSENNYQGNFTAANNL-----PVLIPVTRLPVLARSP-- D +S ++D FG +DI Q+ AN+L P+L+P+ P ++	237	
Sbjct	269	DYISSIADTFGV---DDI-----QSIFDANSISSLSDLIFPFTPLVPLKNPPTRIQTTLS	319	
Query	238	-----SDGRGGI RLPII GISLGCTLLVLA VLLVYVYCLKMKTLMRSASSAE + G + V +G+ +G TLLV++ ++ C K + + + +	287	
Sbjct	320	PPPPKSPVVPNGGADSSKKWVYVGIGATLVLMLPSGII-----CTKKPSYSMENNISL	377	
Query	288	TADKLLSGVGSVYKSKPTM YETDAIMEATMNLSEQCKIGESVYKANIEGKVLAVKRKFEDV + G+ V T+Y+ + + A E +I VY+ I+G A+K K DV	347	
Sbjct	378	SVSS--GGIHHAVESLTVYKYEELOQKAAGFFGEANRIKGCVYRGLIKGDDAAIKMMKGDV	435	
Query	348	TEELKILQKVNHGNLVLGMVSSDNDGNCFVVVEYAENGSLDEWLFSKSCSDTSNSRASL	407	

Sbjct 436 +EE+ IL+ +NH N++L G + GN ++VYEAENGSL +WL +L
Sbjct 436 SEINILKLINHSNVIRSGFCV-HKGNTLVYEAENGSLSDWLHGDG----RIGSTL 489

Query 408 TWQRISMAVDVAMGLQYMHEAYPRIVHRDITSSNILLDSNFKAKIANFSMARTFTNPM 467
W QR+ +A DVA L Y+H P +H++ SNNILLD N + K+ANF +AR N

Sbjct 490 GWKQRVQIACDVANALNYLHNFTNPPIHKNLKSSNILLDGNGRMGVANGLARRLENEE 549

Query 468 MPKIDVFAFGVVLIELLTGRKAMTTKENGEVVMLWKDIWKFIDQEEENREERLKKWMDPKL 527
++D FAFGVV++ELLTG+A + +N E L + ++ + ++ R +L+ ++DP L

Sbjct 550 GGELDAFAFGVVLIELLTGKEAAPS-QNKEGRGLCVSVNEVLEGDDVR-HKLRGFIDPCL 607

Query 528 ESYYPIDYALSLASLAVNCTADKSLSRPTIAEVLSLS 565
YP D A ++A LA +C A +RPT+ +I++ LS

Sbjct 608 THDYPFDLAFTMAQLAKSCIAHDLNARPTMFDLIIILS 645

Score = 78.6 bits (192), Expect = 2e-12, Method: Compositional matrix adjust.
Identities = 43/99 (43%), Positives = 66/99 (66%), Gaps = 5/99 (5%)

Query 469 PKIDVFAFGVVLIELLTGRKAMTT--KENGEVVMLWKDIWKFIDQEEENREERLKKWMDPK 526
PKD+FAFGVV++ELLTG+A + KE GE +L I ++ Q +N ++L+ ++DP

Sbjct 30 PKLIDVFAFGVVLIELLTGKEAAPSQKKEGGE--LLSVSINEVL-QGDNVRDKLRGFIDPC 86

Query 527 LESYYPIDYALSLASLAVNCTADKSLSRPTIAEVLSLS 565
L YP D A S+A LA +C A +RPT+ +I+ LS

Sbjct 87 LAHEYPFDLAFSMAQLAKSCVAHDLNARPTMSDIFVILS 125

>**ref|XP_002269442.1|** PREDICTED: hypothetical protein [Vitis vinifera]
Length=632

GENE ID: 100264999 LOC100264999 | hypothetical protein LOC100264999
[Vitis vinifera]

Score = 268 bits (685), Expect = 1e-69, Method: Compositional matrix adjust.
Identities = 170/583 (29%), Positives = 296/583 (50%), Gaps = 69/583 (11%)

Query 47 SCETYVTYIAQSPNPLSLTNISNIFDTSPSLIARASNLEPMDDKLVKDQVLLPVTCGCT 106
+C+TY+ + ++SP + +++++IS++ + P +A+ +++ + ++ +V PV C C+
Sbjct 54 TCGTYLIFRSSESP-YNNVSSISDLLASDPSQLAQINSVTETA-TFDTNKEVIVPVNCSCS 111

Query 107 GRNSFANISYEINQGDSFYFVATTSYENLTNWRAVMDLNPKLPIGIOQVVFPLFCK 166
GN S N SY + GD + +A + ++ Lt + + + NP +S L G + PL C

Sbjct 112 GNYSQTNTSYVVKNGDYPLWIANNTEFQGLSTCQALLNQNPSVSATNLNPGTSITVPLRCA 171

Query 167 CPSKNQLDKEIKYLITYVWKPGDNVSLSVSDKFGASPEDIMSENNYQGNFTAANNLPVLIP 226
CP+K Q D +KYL++Y+ GD VS +S +FG E + N + T +LIP
Sbjct 172 CPTKAQSDAGVKYLMSYLVAYGDTVSAISGRGVDTERTLEANEALSEQDTINFTTLLIP 231

Query 227 VTRLPVLARS-----PSDRKGKGGIRLPLVIIIGISLGCTLVLVIALV 267
+ P + ++ +K + + V + +L+L +
Sbjct 232 LQNPFPSSSSQTIVPPPPPPPPPSAVSSPSGSSKKTWVYVIVGVAAG---VVVLLFFGYV 288

Query 268 LVVYVCLKMKTLNRSASSAET-----ADKLLSGVSGYVSKPMTYETDAIMEATM 316
+ + K K N + +E+ + + +S +Y+ + AT
Sbjct 289 IFVKFFRKTKKKNDQIAVSESFKPPLKEPLKVEEHEFFESISSMAQSVKVYKFEELQSATD 348

Query 317 NLSEQCKIGESVYKANIEGKVLAJKRFKEDVTEELKILQKVNHNGLVKGNGVSSDNDGNC 376
N S C I SVY+ I+G +A+K+ +V+ E+ +L K+NH N++L G+ NDG+
Sbjct 349 NFSPSCLIKGSVYRGTGKGLAAIKMDGNVSNEIALLSKINHFNVIRLSGICF-NDGHW 407

Query 377 FVYVYEAENGSLDEWLFSKCSSTDNSRASLTWCQRISMAVDVAMGLQYMHEAYPRIVH 436
++V+FEYA NGSL +W++ + N R L W QRI +A+DVA GL Y+H H P +H
Sbjct 408 YLVHEYAVNGSLSDWIIYNN---NDRRFLVWTQRIQIALDVATGLNYLHIHNVSPSYIH 462

Query 437 RDITSSNILLDSNFKAKIANFSMARTFTNP-----MMP-----K 470
+D+ S+N+L LD+F+AKIANF AR+ M P K
Sbjct 463 KDMKSNNVLLDGFRAKIANFDQARSQAEQEGQFALTRHIVGKGYMAPEYLENLISTK 522

Query 471 IDVFAFGVVLIELLTGRKAMTTKENGEVVMLWKDIWKFIDQEEENREERLKKWMDPKLEY 530
+DV+AFGV++E+ TG K + GE + L + + + E++ +E+L + +DP L+
Sbjct 523 LDVYAFGVLMLEIFTG-KEVAALYGGESIHLSEVLAABL-HEDDGKEKLGDIFPSLDGN 580

Query 531 YPIDYALSLASLAVNCTADKSLSRPTIAEVLSLSLQPSP 573
YP + A+ + L +C RP + EIV SLS + S A
Sbjct 581 YPPELAIFMIRLIDSCLTKAPAGRPMDEIVQSLSRILASSQA 623

>**ref|XP_002533279.1|** serine-threonine protein kinase, plant-type, putative [Ricinus communis]
gb|REF29111.1| serine-threonine protein kinase, plant-type, putative [Ricinus communis]
Length=617

GENE ID: 8272991 RCOM_0411670 | serine-threonine protein kinase, plant-type, putative [Ricinus communis]

Score = 265 bits (676), Expect = 2e-68, Method: Compositional matrix adjust.
Identities = 187/601 (31%), Positives = 315/601 (52%), Gaps = 78/601 (12%)

Query 22 FSTNIVAQSQDNRTN----FSCPSDSPPSCETYVTYIAQSPNPLSLTNISNIFDTSPLS 77
+S N+V ++ T F + SC+T++ Y +Q P + +++++IS + + PL
Sbjct 25 YSGNLVMNCNNNDSTGPSPAFLYTCNGKESCKTFLIYKSQPP-YHTVSSISKLTSSDPLE 83

Query 78 IARASNLEPMDDKLVKDQVLLPVTCGCTGNRSFANISYEI-NQGDSFYFVATTSYENLT 136
+A +N+ L ++ ++VP+ C C+ AN SY I + D+++ +A ++YE Lt
Sbjct 84 LALINNISNFT-VLPTNKEVIVIPIICCSSQQYYQANTSIIPISYDFTYFSIAESTYEGLS 142

Query 137 NWRAVMDLNPVLSPNPKLPIGIQVVFPLFCKCPSKNQLDKEIKYLITYVWKPGDNVSLSVSD 196
+M N S L +G++ PL C CP+ NQ KYL+TY GD V VS+
Sbjct 143 TCNSLMRQNN-YSEFSLDVGMLRVLPIRCACPTSNQSANGTKYLLTYSVSGDKVRAVSE 201

Query 197 KFGASPEDIMSENNYQGNFTAANNLPVLIPVTPRLPV-LARSPSDGRK----- 242
+F AS + + NY FT + L P T + V L+ PS +
Sbjct 202 RFNASIDS---NYANGFTKDDT-TLFPFTTILVPLSTEPSSFQTVHYPPPPYSPFF 255

Query 243 ---GGIR-----LPVIIGISLGCTLVLVLAFLVYVYCLKMKTLNRSASSAETA 289

Sbjct	256	IR +PVII +L L ++L L L ++ + E IPVHPIRRSLKKIHWVPIVIIISALPVVLIFVLL--LRNKKSHLGVRKEGKNEELP	313
Query	290	DKLLSGVSGYVSKPTMYETDAIMEATMNLSEQCKIGESVYKANIEGVKVLAVKRKFEDVTE D L V+ +Y + + AT + S ++ +SVY+ I G+VLA+K+ +DV+ Sbjct 314 DDFLDHVAVDGLLKIYTFEELKVATEDFSTSNSRLSDSVYRGVSGQVLAIKKMSKDVSN 373	349
Query	350	ELKILQKVNHNGLVLMGVSSNDGNCFVVYEYAENGSLDEWLFSKSCSDTSNSRASLTW E+ +L+K+NH NL+ L + ++ G +++YE+ +NGSL +WL+ ++C + +W Sbjct 374 EVTLLRKINHFNLLSLH-ACEHHGVFYLMYEFDNGSLRDWLYKRNCLEAQ-----SW 426	409
Query	410	CQRISMADVAMCLQYMHEAYPRIVHRDITSSNILLDSNFKARIANFSMART----- +RI +A+DVA GL Y+H P VH+DI+SSN+LL + +AKIANFS+AR+ Sbjct 427 NRRIQIALDVANGLHYNFTDPPYVHKDISSSNVLLSRHLRAKIANFLSARAKAEHHV 486	462
Query	463	-----FTNP-----MMPKIDVFAFGVVLIELLTGRKAMITTKENGEVVMLWK + P + P+ID++AFGVVL+EL+TG+A+ +E +V L + Sbjct 487 NSSLRLALGSKGYLAPEFIDFGLVTPEDIYAFGVVLELVTGKEAVYMQEERKV-QLSE 545	503
Query	504	DIWKIFDQEENREERLKKWMDPKLESYYPIDYALSLASLAVNCTADKSLSRPTIAEVLS I I ++E N E RL +DP L+S + ++ L + L++ C A + SRP++AEIV + Sbjct 546 TIISIMEKE-NAEARLGCIVDPNLQSQHSMEVVLRMVKLSSLACLAQEPESRPSMAEVSA 604	563
Query	564	L 564 L	
Sbjct	605	L 605	

>ref|XP_002533278.1|  BRASSINOSTEROID INSENSITIVE 1-associated receptor kinase 1 precursor, putative [Ricinus communis]
gb|EEF29110.1| BRASSINOSTEROID INSENSITIVE 1-associated receptor kinase 1 precursor, putative [Ricinus communis]
Length=647

Gene ID: 8272990 RCOM_0411660 | BRASSINOSTEROID INSENSITIVE 1-associated receptor kinase 1 precursor, putative [Ricinus communis]

Score = 265 bits (676), Expect = 2e-68, Method: Compositional matrix adjust.
Identities = 181/601 (30%), Positives = 306/601 (50%), Gaps = 87/601 (14%)

Query	33	DNRTNFSCPSDSPSCETYVTYIAQSPNFLSLTNISNIFDTSPSLSIARASNLEPMDDKLV D+ +SC + SC+TY+T+ +Q P + ++T+IS + ++ P ++ A N	92
Sbjct	42	DSALGYSC-NGLNTSCQTYLTFRSQQPP-YTNVTSISTLLNSDPSQLS-AINSVSETATFD	98
Query	93	KDQVLLVPVTCGCTGNRSFANISYEINQGDSFYFVATTSYENLTNWRAVMDLNPFVLPNPK +++++PVPC+C+G+ AN SY + D+ +F+A +++ L+ +A+ D N + +	152
Sbjct	99	TNKLVIVPVNCSCSGDYYQANTSYYVQAKDAPFFIANNTFQGSLSTCQAINDQNRRQTVDI	158
Query	153	LPIGIQVVFPLFCPSKNQLDEIKYLITYWKPGENVSLVSDKFGASPEDIMSENNYG P I + PL C +KNQ D IKYL++Y+ GD VS VS KFG + + N	212
Sbjct	159	FPNEI-LHIPLRCACPKNQTDAGIKYLLSYLWTWGDITVSAVSVKFGGNTGRSLEANGLS	217
Query	213	-QNFTAANNLPLVLIPLVTRLPV-----LARSPSDGRKGIGRLPVIIG Q T +LIP+ P +P++G + V+G	252
Sbjct	218	EQTPTIYPFTTLPPTSNQTISPPPPPASSTPNNGSSKKWVYLVG	277
Query	253	ISLGCTLLVLVLAVLVVYVYCL-----KMKTLNRSASSAETADKLL + G +V L ++ + Y L + K+LN+ E + L	293
Sbjct	278	VLAG---IVFTLGLVTIIFYALFRRSKRKEPEPIIVSESFEAQEKSLSNKLD--EESQDFL	332
Query	294	SGVSGYVSKPTMYETDAIMEATMNLSEQCKIGESVYKANIEGVKVLAVKRKFEDVTEELKI +S +Y+ + + AT N S C I SVY+ I G A+K+ DV++E+++	353
Sbjct	333	DSIISIAQSIKVYKFKELEATDNFSPSCKWIKGSVYRGYISGDAYAIKKVNGDVSKEIEL	392
Query	354	LQKVNHNGLVLMGVSSNDNCNFVYVEYAENGSLDEWLFSKSCSDTSNSRASLTWCQRI L KVHN NL++L GV G+ ++VYEA NG+L +W++ ++N L+W QR+	413
Sbjct	393	LNKVNHFNLIRLSGVCFSG-GHWLVLYVEYAANGALSDWIY---SNNEGNFLSWTQRV	446
Query	414	SMAVDVAMGLQYMHHEAYPRIVHRDITSSNILLDSNFKAKIANFSMARTFTNP----- +A+DVA GL Y+H P +H+DI SSN+L+DS+F+AKIAN +MAR+	466
Sbjct	447	QIALDVTAGLNYLHSFTSPPHIHKDIKSSNVLIDSDFRAKIANLAMARSTEGQDGEGFALT	506
Query	467	-----MMP-----KIDVFAFGVVLIELLTGRK--AMTTKENGEVVMLWKDI M P K+DV+AFG++E++T+G+ A+ T+EN + + D+	505
Sbjct	507	RHIVGTGYMAPEYLENLGVSTKLDVYAFGILMLEMVTGKEVAALYTEENLNLSDIINDV	566
Query	506	WKIFDQEENREERLKKWMDPKLESYYPIDYALSLASLAVN-CTADKSLSRPTIAEVLSL +E+ ++ LK++DP +E +P + +L + ++ C RP + EI SL	564
Sbjct	567	LS---KEDGQQSLKQFVDPSENFPSEISLFFMMVRMIDSCLNKNPADRPAMDEISQL	622
Query	565	S 565 S	
Sbjct	623	S 623	

>ref|XP_002269408.1|  PREDICTED: hypothetical protein [Vitis vinifera]
Length=638

Gene ID: 100242712 LOC100242712 | hypothetical protein LOC100242712
[Vitis vinifera]

Score = 263 bits (673), Expect = 4e-68, Method: Compositional matrix adjust.
Identities = 176/574 (30%), Positives = 293/574 (51%), Gaps = 66/574 (11%)

Query	47	SCETYVTYIAQSPNFLSLTNISNIFDTSPSLSIARASNLEPMIDKLVKDQVLLPVTCGCT SC+ ++ + + P + ++IS++ + P +A+ +++++ K +V+ VEV C C+	106
Sbjct	54	SCQAFLIFRSEPP-YNDVSSISDLGSDPSQLAQINSVDETATFETKKEVI-VPVNCSCS	111
Query	107	GNRSFANISYEINQGDSFYFVATTSYENLTNWRAVMDLNPFSPNKLPIGIQVVFPLFCK G S AN SY + GD++ +A ++E L+ -A+ L+ N + G ++ PL C	166
Sbjct	112	GEFSQANTSYVQHGDTLYLNIANTTFEGLSTCQALRSQRTSLTTN-IYTGTKLTVPLRCA	170
Query	167	CPSKNQLDKEIKYLITYWKPGENVSLVSDKFGASPEDIMSENNYG-QNFTAANNLPLVLI CP+KNQ D +Y+ GD VS +S +FG + N QN +LI	225
Sbjct	171	CPTKNQSDVGVKYLMSYLVASGDYVSSISVRFVDTGMTLEANELSEQNPNIYPFTLLI	230
Query	226	PVTRLP-----VILARSPSDGRKGIGRLPVIIGSL-----GCTLLVLVLAVAL	267

Sbjct	231	P+ LP ++ P PLQNLPSQSQTIVPPPPPPSPPPPATAVSSPSKSLKKTWVYVVGVVAGSALVLLFGSVI	SL	G L++L +V+	290
Query	268	LVYVYCLKMKTLNRSASS-----	AETADKLLSGVSGYVSKPTMYETDAIMEATMN	317	
		+ K + AS E + L +S +Y+ + + AT N			
Sbjct	291	FFKFRKRKTKTDPIAISESFEACEKPLKEEQHFLIESISSIAQSLKVYKFEELQSATDN			350
Query	318	LSEQCKIGESVYKANIEGKVLAVKRFKEDVTEELKILQKVNHGNLVKLMGVSSNDGNCF			377
		S C+I SVY+ I+G + A+K+ +V+ E+ +L K+NH N++L G+ NDG+ +			
Sbjct	351	FSPNCRIKGSVYRGTIKGDAAIKMDGEVSNEIALLNKINHNFNVIRLSGICF-NDGHWY			409
Query	378	VVYYAENGSLDEWLFSKSCSDTSNSRASLTWCQRISMAVDVAMGLQYMHEAYPRIVHR			437
		+V+EYA NG L +W++ + +SR L W QRI +A+DVA GL Y+H + P VH+			
Sbjct	410	LVEHEYAVNGPLTWIYN---NNDDSRF-LVWMQRIOQIALDVATGLNYLHSYTSPPYVHK			464
Query	438	DITSSNILLDSNPKAKIANFSMARTFTNP-----	MMP-----	KI	471
		DI S N+LLDS+F+AKIANF +AR+ M P K+			
Sbjct	465	DIKSGNVLLSDSFRAKIANFGLARSAEGQEGQFALTRHIIGTRGYMAPEYLENGLVTKL			524
Query	472	DVFAFGVVLIELLTGRKAMTTKENGEVVMLWKIDIWKIFDQEENREERLKKWMDPKLESYY			531
		DV+AFGV++E+LTG++ E GE + L D+ E + +E+L+ ++DP L Y			
Sbjct	525	DVYAFGVLMLEMGTKEVAALY-EGENMHL-PDVLVAVLHEGDGKEKLRNFIDPSLSGNY			582
Query	532	PIDYALSLASLAVNCTADKSLSRPTIAEIVLISL 565			
		P++ A+ + L +C SRP + EIV +LS			
Sbjct	583	PLELAIVMIRLIDSCLKKSPASRPDMVEIVQALS			616

>ref|XP_002327712.1| predicted protein [Populus trichocarpa]

gb|EEE75190.1| predicted protein [Populus trichocarpa]

Length=630

GENE ID: 7464252 POPTRDRDRAFT_796841 | hypothetical protein [Populus trichocarpa] (10 or fewer PubMed links)

Score =	258 bits (658), Expect = 2e-66, Method: Compositional matrix adjust.
Identities =	181/588 (30%), Positives = 297/588 (50%), Gaps = 90/588 (15%)
Query	47 SCETYVTTYIAQSPNFLSNTNISNI FDTSPLSIARASNLEPMDDKLVKDQVLLPVTCGCT 106
	SC+ Y+ + +Q P + ++ +IS + + P ++ +++ +Q++ +VPV C C+
Sbjct	42 SCQAYLIFRSQP-YNTVASISTLLGSDPSQLSEVNSETT-SFPSNQLVIVPVNCSCS 99
Query	107 GNRSFANISYEINQGDSFYFVATTSYENLTNWRAVMDLNPNVLSPNKLPIGIQVVFPFLCK 166
	G S AN SY + D+ + A+ +Y+ L+ +A+ + + + L G + PL C
Sbjct	100 GEYSQANASYIVQPNDTFLIANNTYQGLSTCQALQNQKTTRTDDILS-GETLTVPLRCA 158
Query	167 CPSKNQLDKEIKYLITYVWKPGDNVSLVSDKFGASPEDIMSENNY-GQNFTAANNLPVLI 225
	CP+KNQ D I+YL++Y+ PGD+V +S++FGA+ + N ON T +LI
Sbjct	159 CPTKNQSDLGIRYLLSYLWTGDDVPAISEQFGAATGRTLEANGLPEQNPTIPFTTLLI 218
Query	226 PVTRLPVLARS-----
	PSDGRKGIGRLPVVIGISLG 256
Sbjct	219 PLQSTPTSSQTVVPPPPPAPSSSPSPSPNPEKSSKKTWTLYVVVGVVGIIATLIVIG--- 274
Query	257 CTLLVVLIA-----
	VLLVYVYCLKMKTLNRSASSAETADKLLSGVSGYVSKPTMYE 307
	T++ +L+ V+ + +K LN+ E + + +S +Y+
Sbjct	275 -TIIFFMLSRSKSQGPVIESQSFQEAHEKPLNKLD--EESQEFFFESISAQSIKVYK 331
Query	308 TDAIMEATMNLSEQCKIGESVYKANIEGKVLAVKRFKEDVTEELKILQKVNHGNLVKLMG 367
	+ + AT N S C I SVY+ I G A+K+ DV++ +++L K+NH NL++L G
Sbjct	332 FEDLKAATDNFSPSCLKGVSVYRGLINGDFAAIKMMNGDVSKEIENNINHNSLIRLSG 391
Query	368 VSSDNDGNCFVVYEEAENGSLDEWLFSKSCSDTSNSRASLTWCQRISMAVDVAMGLQYMH 427
	V NDG+ ++VYEEYA +G L -W++ D SN L W +RI +A DVA GL Y+H
Sbjct	392 VCF-NDGHWLYVYEEAASQQLSDWIY----DRSNEGKFLNWTKRIQIASDVATGLNYLH 445
Query	428 EHA-YPRIVHRDITSSNILLDSNPKAKIANFSMARTFTNP-----
	MMP- YP VH+DI SSNILLDS+ +AKIANFS+AR+ + M P
Sbjct	446 SFTNYPH-VHKDKSSNILLDSLRAKIANFSLARSTGDQDFEVLTTRHVGKGYMAPE 504
Query	470 -----KIDVFAFGVVLIELLTGRK--AMTTKENGEVVMLWKDIWK-IFDQEENREE 517
	K+DV+AFG++ +E++TG++ A+ ++E+ + D+ + + +EE
Sbjct	505 YLENGVVSQSKLDVYAFGILTLEIITGKEVAALHSEESRNLI---SDVLNGALSEVDGQEE 560
Query	518 RLKKWMDPKLESYYPIDYALSLASLAVNCTADKSLSRPTIAEIVLSSL 565
	LK+ +DP L YP A+ + L +C RPT+ EIV SLS
Sbjct	561 SLKQLIDPSLHENYPSGLAVLVRLLIDSCLNKNGDRTMDEIVQSL 608

>ref|XP_002310777.1| predicted protein [Populus trichocarpa]

gb|EEE91227.1| predicted protein [Populus trichocarpa]

Length=643

GENE ID: 7477999 POPTRDRDRAFT_563086 | hypothetical protein [Populus trichocarpa] (10 or fewer PubMed links)

Score =	254 bits (649), Expect = 2e-65, Method: Compositional matrix adjust.
Identities =	180/586 (30%), Positives = 289/586 (49%), Gaps = 84/586 (14%)
Query	47 SCETYVTTYIAQSPNFLSNTNISNI FDTSPLSIARASNLEPMDDKLVKDQVLLPVTCGCT 106
	SC+ Y+ + +Q P + ++ +IS + + P ++ +++ +Q++ +VPV C C+
Sbjct	53 SCQAYLIFRSQP-YNTVASISTLLGSDPSQLSINSVSETTS-FPTNQLVLPVNCSCS 110
Query	107 GNRSFANISYEINQGDSFYFVATTSYENLTNWRAVMDLNPNVLSPNKLPIGIQVVFPFLCK 166
	G+ AN SY + G++ + A+ +Y+ L+ +A+ + + +N G + PL C
Sbjct	111 GDYFQANASYIVQSGNTFLLIANNTYQGLSTCQAIRNEKGTRTNIFA-GETLTVPLRCA 169
Query	167 CPSKNQLDKEIKYLITYVWKPGDNVSLVSDKFGASPEDIMSENNYGQ-NFTAANNLPVLI 225
	CP+KNQ D I+YL++Y+ GD VS+ +FGA+ + N + N T +LI
Sbjct	170 CPTKNQSDLGIRYLLSYLWTGDDVSIAGVRFGADIGRALEANEISEKNPTIYFPTTLLI 229
Query	226 PVTRLPVLARS-----
	PSDGRKGIGRLPVVIGISLG 266
Sbjct	230 PLKNPPTSSQTVVPPPPPAPSPSPSPSPNSDKSANKTWTIYVFVG-AVGGIVLTLVIGT 288

Query	267	LLVVYVYCLKMKT-----LNRASSAETADKLLSGVSGYVSKPTMYETD ++ ++ K K LNR E LL V +Y +	309
Sbjct	289	IIFFMLFRKSKKQPGPIIVSQSFEAHKPLNRKLD--EEPQDILLESVSYIAQSIVNYE	346
Query	310	AIMEATMNLSEQCKIGESVYKANIEGKVLAVKRFKEDVTEELKILQKVNHGNLVKIMGVS + AT N S I SV++ I G A+K+ DV++E+ +L K+NH NL++L GV	369
Sbjct	347	DLKAATDNFSPSFVIKGSVFRGLINGDFAAIKKMNQDVSKIEDLLNKINHSNLIRLSGVC	406
Query	370	SDNDGNCFVYYEYAENGSLDEWLFSKSCSDTSNSRASLTWCQRISMAVDVAMGLQYMHEH NDG+ ++VYEYA NG L +W++ +SN L W QRI +A DVA GL Y+H	429
Sbjct	407	F-NDGHWLYVYEYAANGPLSDWIYV---SSNEGKFLWTQRIQIATDVATGLNLYLHSF	460
Query	430	A-YPRIVHRDITSSNILLDSNFAKIANFSMARTFTNP-----MMP--- YP VH+DI SSNI LD + AKIANFS+AR+ P M P	469
Sbjct	461	TNYPH-VHKDIKSSNILLDKDLRAKIANFSLARSTDGPEGEFALTRHIVGTTKGYMAPEYL	519
Query	470	-----KIDVFAGVVILI LITGRK--AMTTKENGEVVMLWKDIWK-IFDQEENREERL K-DV+AFG++ E++TG++ A+ +EN E+ D+ + +E EE L	519
Sbjct	520	ENGIICTKLDVYAFGILTLEMTGKEVAALYREENREI---SDVLNGVLSEEGGLEESL	575
Query	520	KKWMDPKLESYYPIDYALSLASLAVNCTADKSLSRPTIAEIVLSSL 565 + +DP ++ YP A+ + L +C RP + EIV SLS	
Sbjct	576	SQLIDPSMQGNYPGSLAVLVMVRIDLSCLNKPAGRPMAMDEIVQSL 621	

>ref|XP_002281880.1| PREDICTED: hypothetical protein [Vitis vinifera]
Length=622

GENE ID: 100248852 LOC100248852 | hypothetical protein LOC100248852
[Vitis vinifera]

Score = 253 bits (647), Expect = 4e-65, Method: Compositional matrix adjust.
Identities = 178/567 (31%), Positives = 289/567 (50%), Gaps = 62/567 (10%)

Query	47	SCETYVTYIAQSPNFSLTNISNIFDTSPLSIARASNLEPMDDKLVKDQVLLPVTCGCT SC+ ++ + ++ P + S+ IS + ++P +AP + + + + +V+ VPV C C	106
Sbjct	54	SCQAFLIFKSEPP-YNSVPTISMSSNPGELARINSVKTLTVPFTGKEVI-VPVNCSCL	111
Query	107	GNRSFANISYEINQGDSFYVF-ATTSYENLTNWRAVMDLNPVLSPNKLPIGIQVVFPLFC G AN ++ I YF+ +Y+ L+ +M N S L G++ PL C	165
Sbjct	112	GQQYQANTTFHIQDNQQTYYIFIQNNNTYQGLSTCDSLMRANR-YSEFSLSPGLELHVPLRC	170
Query	166	KCPSKNQLDKEIKYLITYVWKPGDNVSLVSDKFGASPEDIMSENNEY--QONFTAANNLPV C +++Q + KYL+TY DN + ++F S + I N +N T +	223
Sbjct	171	ACHTEHQAENGTKYLITYSVSWEDNFTPPTIGERFNVSAKSIADANGLISEENPTIFPFPTT	230
Query	224	LIPVTRLPVALAR-----SPSDGRKGGGIRLPVIIIGISLGCTL--VLVL LIP+ P+ ++ S S + R+ + GI+ GC LL V+	264
Sbjct	231	LIPLKTEPLSSQTKTHATQPVLDPPPPSTS DSGSSRSKRRIYLGAGIAAGCFLLGPSVIFS	290
Query	265	AVLLVYVYCLKMKTLNRSASSAETADKLLSGVSGYVSKPTMYETDAIMEATMNLSEQCKI V L Y K + + + LL ++ P ++ + +AT N S + +I	324
Sbjct	291	IVFLFYKKRSKVKPPVHGTKSVPEDLLVEIASVDPVVKFEEKKLKKATGNFSSKSRI	350
Query	325	GESVYKANIEGKVLAVKRFKEDVTEELKILQKVNHGNLVKLMGVSSDNDGNCF-VVYEYA V++A + ++AVK+ K D++EE+ IL K+NH NL+KL GV +G+CE +V+EY	383
Sbjct	351	KGCVFRAELGREIYAVKRMKVDISEEVNILNKNHNCNLKIHGVC--KNGSCPYLVFYM	408
Query	384	ENGSLDEWLFSKSCSDTSNSRASLTWCQRISMAVDVAMGLQYMHEHAYPRIHRDITSSN ENGSL EWL +S S +W +RI +A+DVA GL Y+H P VH+ I SNN	443
Sbjct	409	ENGSLREWLHKESS---SNHSQSWSKRIQIALDVAHLHYIHNFTKPAYVHVKHIKSSN	462
Query	444	ILLISNFKAKIANFSMART-----FTNP-----MMPKIDVFAFG ILL N +AKIANFS+ART + P + PE+DV+AFG	477
Sbjct	463	ILLTKNLRKIANFSLARTAVKGAKTHALNMLVVGTRGYMAPEYIEAGSITPKVDVYAFG	522
Query	478	VVIELLTGRKAMTTKENGEVVMLWKDIWKIFDQEENREERLKKWMDPKLESYYPIDYAL VV++EL+TG+ A+ +N E V+L + + I ++ N E L ++DP L I+ A	537
Sbjct	523	VVMLELITGKDAVII-QNEEVLLSEAMISIMER-GNAEIELGHFLDPCLLGNNNGIESAT	580
Query	538	SLASLAVNCTADKSLSRPTIAEIVLSSL 564 +A L++ C RP++ E+V +L	
Sbjct	581	RIAKLSIACLTKDQARRPSMGEVVSTL 607	

>ref|XP_002509540.1| ATP binding protein, putative [Ricinus communis]
gb|REF50927.1| ATP binding protein, putative [Ricinus communis]
Length=681

GENE ID: 8271475 RCOM_1677900 | ATP binding protein, putative
[Ricinus communis]

Score = 253 bits (647), Expect = 4e-65, Method: Compositional matrix adjust.
Identities = 201/621 (32%), Positives = 299/621 (48%), Gaps = 104/621 (16%)

Query	44	SPSPCETYVTYIAQSPNFSLTNISNIFDTSPLSIARASNLEPMDDKLVKDQVLLPVTC S C+T+ ++ + F SL+N+S + IA A+ + L KQD LL+P+ C	103
Sbjct	49	SQDHCKTFAI-LSTNSYFSSLSNLSFYLGPNRFVIAEANGFSADTEFLPKDQPLIPDC	107
Query	104	GCTGNRSFANISYEINQGDSFYFVATTSYENLTNWRAVMDLNPVLSPNKLPIGIQVVFPL C GN A ++ +G++FY +A S E LT +A+ + N +SP L ++++ PL	163
Sbjct	108	KCNGNFFRAEVTKTIKGENFYGIAE-SLEGITCKAIQENNGLVSPWNLADKARLLVPL	166
Query	164	FCKCPSKNQLDKEIKYLITYVWKPGDNVSLVSDKFGASPEDIMSENNEY-QNFTAANNLP C CPS +Q+ ++L+Y GD +S ++ KF +PE I+S NN NF N +P	222
Sbjct	167	RCACFSSSVQTLATRFLLSYPVSEGDTISNIAKFNTTPAEIISANRSLANFKPENLVP	226
Query	223	--VLPVTRLPVLA----RSP-SDGRKGGGIRLPV-----IGISLGCTL-- +LIP+ R P L R P S R+ I PVI IG+ + T +V	261
Sbjct	227	LASLLIPLRNPAALGSLAKPREPNSPFPRESSI--PVINPHKKSKMWNIGVYIAVTGVVV	284
Query	262	-----LVLAVLIVVYVYCLKMKTLNRSASSAETADKLLS--GVSGYVSKPTM +V A L+V + K +L+ S S T+K +S G + +	305
Sbjct	285	GATIAIVAAFLIVQLKKKKQNLSKDGDPELQLQLSLSVRTTSEKKVSFEGSQDLDNQII	344
Query	306	-----YETDAIMEATMNLSEQCKIGESVYKANIEGKVLAVKRFKEDVTEELK	352

Sbjct	345	Y + + +AT+ S I SVY + GK LA+KR K + ++ DTPPRNRKVLVENYTVEELRKATEDFSSSLIDGSVYGRNLNGKNLAIKRTKSETISKID	404
Query	353	IILQKVN----HGNLVKLMGVSSNDNGNCVFVVEYAENGSLDEWL-----FSKSCSD N H++L+G + F+V+EYA+N GSL +WL F SC	399
Sbjct	405	FSHFQNATHHHPNIIRLLGTCLSEGSDSFLVFEYAKNGSLKDWLHGGLAMKNQFIASC--	462
Query	400	TSNSRASLTWCQRISMAVDVAMGLQYMH EAYPRIVHRDITSSNILLDSNFKAKIANFSM LTW QR+ +DVA+ LQYMH P VHR++ S NI LD F AKI NF M	459
Sbjct	463	---YCFLTNQRLKICLDVAVALQYMH HIMNPYSVYHRNVKSRSNIFLDEEFNAKIGNFGM	518
Query	460	ARTF-----TNP-----MMPKIDVFAFGVVLIELLTGRKAMT AR TNP + P ID+FAFGVVL+E+L+G++ +T	491
Sbjct	519	ARCIEGDTQNTIEIHSTNPSSWSLGYLAPEYIHQGIVSPCIDIAFGVVLLEVLSGRKRPIT	578
Query	492	TKEN-GEVVMLWKDIWKFIDQEENREERLKKWMDPKLESYYPIDYALSLASLAVNCTADK +N GE L + K EN E L+WMD L Y D A++LA+IA +C ++	550
Sbjct	579	RPDNKGEESNLSEKMKSISSNAGE-LREWMNDNALGENYSFDATVTLANLARSCVEEE	637
Query	551	SLSRPTIAEIVLSSLTLPQS 571 RP E+V LS L + S	
Sbjct	638	PSLRPNADELVEKLRSRIVEES 658	

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>ref|NP_001058110.1| [ORZ] Os06g0625200 [Oryza sativa Japonica Group]
  dbj|BAD35689.1| [ORZ] receptor protein kinase-like [Oryza sativa Japonica Group]
  dbj|BAD37734.1| [ORZ] receptor protein kinase-like [Oryza sativa Japonica Group]
  dbj|BAF20024.1| [ORZ] Os06g0625200 [Oryza sativa Japonica Group]
  gbi|EAZ37689.1| [ORZ] hypothetical protein OsJ_22029 [Oryza sativa Japonica Group]
Length=630
```

GENE ID: 4341567 Os06g0625200 | Os06g0625200 [Oryza sativa Japonica Group]
(10 or fewer PubMed links)

Score = 251 bits (640), Expect = 3e-64, Method: Compositional matrix adjust.
Identities = 170/578 (29%), Positives = 297/578 (51%), Gaps = 86/578 (14%)

Query	47	SCETYVTYIAQSPNFLSLTNISNIFDTSPLSIARASNLPEMDDKLVLVKDQVLLVPVTCGCT	106
Sbjct	56	SC S C Y+T+ + P +++ + + + P ++A A+++ + Q+LLVPV C C	109
Query	107	SCTAYLTFRSDPPP----LSVAYLNATPSAAVAANSPVLAQSPVDTQQLLVPVPCSC-	162
Sbjct	110	-NRATGYQQHNTTYA1QEDTFFLIANNTFQGLTTYQSIIAANNPASEAMSPVINGPLAVP	168
Query	163	LFCKCPSKNQLDKEIKYLITYWVKPGNDNSVLSVDKIGASPEDIMSENYYGNQNFTAANNLP	222
Sbjct	169	L C CPS I L+TYV + GDNV + +F++ D++ N	214
Query	223	VLIPVTRLP-----VLARSPSDGRK-----GGIRLPLVIIGISLGCTLLVVL	264
Sbjct	215	+L+P+ P + + +P + +K G+ + IGT G+ VL	274
		LLVLPVHPHSRVVLANITITSTTPESQKFYVSSPCSNGLLAGLGIYVGCGVSAAWAL	
Query	265	AVLVLVYVYCLKMKTLNRSASSAETADKLLSGVGSGYVSKPTMYETDAIMEATMLNSEQCKI	324
Sbjct	275	AV L++ + + S + ET L++ V G V Y I AT +E+ ++	332
		AVFLLWRRRRRPVGDSGMARET--PLVAARVGAETLAAYSYADIETATAGFAEERRV	
Query	325	--GESVYKANIEGKVLAVKRFK---EDVTEELKILQKVNHNGLVLMGVSSDNDGNCFVV	379
Sbjct	333	G SVY+A I G+ AVKR +DV E+ +L +VNH LV+L G+ ++ D + ++V	391
Query	380	YEYANGSLDEWLFSKSCSDTSRNSRLSTWQCRISSMAVDVAMGLQYMHEHAYPRIVHRDI	439
Sbjct	392	E+AENG+L EWL S + + R L W QR+ +A+DVA GL Y+H P VH+++	449
		LEFAENGALSEWLHPGSAA--ACLRRLVLGKQRVLVALDVAGGLNYLHHFTNPVYHKNL	
Query	440	TSSNILLDSNFKA KIANFSM-----ARTFTNP-----MM	468
Sbjct	450	S N+L+D+N +AK++ + + +P + +	509
Query	469	PKIDVFAGVVLIELLTGR-KAMTTKENGVEVMLWKDIWKFIDQEEENREERLKKWMDPKL	527
Sbjct	510	PK+DVF+FGV+ +ELL+G+ A T + +G+ ++LW+ +D + +L+ +MDP+L	568
Query	528	ESYYPIDYALSLASLAVNCTADKSLSRPTIAEIVLSLS	565
Sbjct	569	+ +YPI A ++A+LAV C A + +RF+ E+ ++LS QGHYPIGAVASALAVRCVAREPRARPSMEEVFTLS	606

>**ref|XP_002307830.1|** predicted protein [Populus trichocarpa]
gb|EEE94826.1| predicted protein [Populus trichocarpa]
Length=659

GENE ID: 7479122 **POPTRDRAFT_862283** | hypothetical protein [Populus trichocarpa]
(10 or fewer PubMed links)

Query	268	LVVYVYCLKMKTLNRSASSAETADKLLSGVGSGYVSKP-----	TMY	306
		+ K + + S+E + L S + + P	T+Y	
Sbjct	296	GFLFWHRKSRKQQPKVSTSE-PETLPSVSTDFTVLPVSNNKSWSLSSHDARYAIESLTVY		354
Query	307	ETDAIMEATMNLSEQCKIGESVYKANIEGKVLAVKRFKEDVTEELKILQKVNHGNLVKLM		366
		+ + + AT ++ I SVY+ + G AVK K DV+ E+ IL+ +NH N++L		
Sbjct	355	KYEDLQVATGYFAQANLIKGSVYRGSFKGDTAAVKVVKGDSVSEINILKMINHSNVRILS		414
Query	367	GVSSDNDGNCFVWVYEYAENGSLDEWLFSKSCSDTSNSRASLTWCQRISMAVDWAMGLQYM		426
		G ++GN ++VEYA+NGSL +WL S +N L W QR+ +A DVA L Y+		
Sbjct	415	GFCI-HEGNTYLVYADNGSLTDLWS-----NNIYRILAWQQRVRIAYDVADAINYL		467
Query	427	HEHAYPRIVHRDITSSNILLDSNFKAKIANFSMARTFTNP-----		466
		H + P +H++ +SNILLD+N +AK+ANF +ART N		
Sbjct	468	HNUTNPSYIHKNLKTNSNILLDANLRAKAVANFGTLARTLENGQDGLQLTRHVVGTQGYLAP		527
Query	467	-----MMPKIDVFAFGVVLIELLTGRKAMTT---KENGEVVMLWKDIWKFIDQEEENRE		516
		+ PK+DVFAGVV++ELL+G+A T K G+ +L I ++ +N		
Sbjct	528	EYIENGVITPKLDFVAFGVVMLELLSGKEAAAATIDKIAGD-DLLSVMIMRVL-EGDNVR		585
Query	517	ERLKWWMDPKLESYYPIDYALSLASLAVNCTADKSLSRPTIAEIVLSLS		565
		E+L ++DP L YP+D A S+A LA +C +RP++ ++ + LS		
Sbjct	586	EKLSAFLDPCLRDEYPLDIAFMSAQLAKSCVEHDLNTRPSMPQVFMMMS		634

>emb|CA002961.1| LysM-domain containing receptor-like kinase [Medicago truncatula]
var. truncatula]
Length=131

Score = 240 bits (613), Expect = 4e-61, Method: Composition-based stats.
Identities = 111/130 (85%), Positives = 121/130 (93%), Gaps = 0/130 (0%)

Query	412	RISMAVDVAMGLQYMHEHAYPRIVHRDITSSNILLDSNFKAKIANFSMARTFTNPMMPKI	471
		RI++A+DVA+GLOQMHEH YPR+HRDIT+SNILL SNFKAKIANF MART TN MMPI	
Sbjct	1	RITIAMDVAIGLOQMHEHTYPRIIHRDITTSNILLGSNFKAKIANFGMARTSTNSMMPKI	60
Query	472	DVAFAGVVLIELLTGRKAMTTKENGEVVMLWKDIWKFIDQEEENREERLKKWMDPKLESYY	531
		DVAFAGVVLIELLTG+KAMTTKENGEVV+LWKD WKIFD E NREERL+KWMDPKLES+Y	
Sbjct	61	DVAFAGVVLIELLTGKAMTTKENGEVVILWKDFWKIFDLEGNREERLRKWWMDPKLESFY	120
Query	532	PIDYALSLAS 541	
		PID ALSLAS	
Sbjct	121	PIDNALSLAS 130	

>ref|XP_002300098.1| predicted protein [Populus trichocarpa]
gb|EEE84903.1| predicted protein [Populus trichocarpa]
Length=680

Gene ID: 7467712_POPTRDRAFT_641782 | hypothetical protein [Populus trichocarpa]
(10 or fewer PubMed links)

Score = 238 bits (607), Expect = 2e-60, Method: Compositional matrix adjust.
Identities = 196/650 (30%), Positives = 304/650 (46%), Gaps = 104/650 (16%)

Query	14	IILCLVIMLFSTNIVA-QSQODNRNTNFSCPSDS-PPSCETYVTYIAQSPNFLSLTNISNIF	71
		++CL++ N+++ Q+ + + C S+ C+T+ + S F SL+N+S	
Sbjct	19	LICLLVSAALQNLNSCPLQTSPDAGYHCNSNGNLQDQCKTFAI-LHTSSYFSSLNSLNFYL	77
Query	72	DTSPLSIARASNLEPMDDKLVKDQVLLPVTCGCTGNRSFANISYEINQGDSYFVWATTS	131
		IA + + + L KDO LL+P+ C C G A ++ +G+SFY ++ S	
Sbjct	78	GLDRFVIAATNGFSANTEFLPKDQPLLPIDCKCNGGGFQALVTKTTIKGESFYSI-SKS	136
Query	132	YENLTNWRAVMDLNPLVSPNPKLPIGIVQVFPLFKCPSKNQLDKREIKYLITYVWKPQGDNV	191
		E LT +A+ + NP +SP L +Q+ PL C CPS ++ + L++Y GD +	
Sbjct	137	LEGLTTCKAIREKNGPGISOPENLNKGKVLQVPLRACAPSSTEVILATRLLSYPVSAGDTI	196
Query	192	SLVSDKFGASPEDIMSENN-----YGQNFT-----AANNLPVL-IP	226
		S ++ KF +PE I S NN G T A N P L IP	
Sbjct	197	SNLAIKFNTTPPEAITSANRNSLTTFKPDSLVLTSLLIPLGGKPTLGPLAKPNEPNLHIP	256
Query	227	VTRPLVLLARSPSDGRKGIGIRLPVIIGISLGCILVLLVLAFLVYVYCLMKMTLNRSASSA	286
		+ LPV+ +P R R+ V I ++ + +A + + K K + +	
Sbjct	257	ASSLPVI--NPHKKRSKMWIGRIVGYIAVTGAVVGSIAAAFLVIQLKKKQVLSKEADT	314
Query	287	E-----TADKLLS---GVSGYVSKP-----MYETDAIMEATMNLSEQCK	323
		E +DK +S + + + S+ T Y + + AT + + +	
Sbjct	315	ELQQLSLSVRTTSDKKVFSDDSNHFDQSITDTPGKVFVETTYVEELKRATEDFNSSNQ	374
Query	324	IGESVYKANIEGKVLAVKRFKEDVTE--ELKILQKV--NHGNLVKLMGVSSDNDGNCFVV	379
		I SVY + GK LA+KR + + EL + Q +H N+++++G + F+V	
Sbjct	375	IEGSVYHGRLNGKLNALKRVQPETISKVELGGLFPQDATHHHPNITRUVGTCLEGPDSFLV	434
Query	380	YEYANGSLEDWL-----FSKSCSDTSNSRASLTWCQRISMAVDWAMGLQYMHEHA	430
		+EYA+NGSL +WL F SC LTW QR+ + DVA+ LQYMH	
Sbjct	435	FEYAKNGSLKDWLHGLAMKNQFIASC-----YCFLTNQRLKICLDAVALQYMHIM	488
Query	431	YPRIVHRDITSSNILLDSNFKAKIANFSMART-----TNP-----MMPI--	470
		+P VHR+I S NI LD F AKI NF MA TNP + P+	
Sbjct	489	HPSYVHRNIKSRNIFLDEFNAKIGNFGMAGCVERDDTKEPDFNSTNPASWLSGYLAPEAH	548
Query	471	-----IDVFAFGVVLIELLTGRKAMTT-KENG-EVVMLWKDIWKFIDQEEENREERLKK	521
		D+F+FGVVL+E+L+G+ +T +NGE + L K I I EN +E L++	
Sbjct	549	QGVSSSSTDIFSGVVLMEVLSQGTPITRPNNDNGEGSIWLSKKIKSIL-LSENADE-LRE	606
Query	522	WMDPKLESYYPIDYALSLASLAVNCTADKSLSRPTIAEIVLSLSSLTQPS	571
		W+D + Y D A +LA+A CT + RPT EIV L L + S	
Sbjct	607	WIDSAMGENYSFDEAATLANIARACTEEDPSLRLPTSGEIVEKLLRLVEES	656

>ref|NP_566689.2| CERK1 (CHITIN ELICITOR RECEPTOR KINASE 1); kinase/ receptor signaling protein/transmembrane receptor protein kinase [Arabidopsis thaliana]

dbj|BAF92788.1| chitin elicitor receptor kinase 1 [Arabidopsis thaliana]

Length=617

Gene ID: 821717 CERK1 | CERK1 (CHITIN ELICITOR RECEPTOR KINASE 1); kinase/receptor signaling protein/ transmembrane receptor protein kinase [Arabidopsis thaliana] (10 or fewer PubMed links)

Score = 236 bits (602), Expect = 8e-60, Method: Compositional matrix adjust. Identities = 163/535 (30%), Positives = 270/535 (50%), Gaps = 74/535 (13%)

Query 89	DKLVKDQVILLPVPTCGCT-GNRSFANISYEINQGDSFYFVATTSYENLTNWRAVMIDLNPV	147
D++	+LVP C C G+ N SY + Q D++ VA +Y NLT ++ NP	
Sbjct 77	DRIQMGSRVLVPFCPECQPCDFLGNFSYSVRQEDTYERVAISYANLTMEISLQARNPF	136
Query 148	LSPNKLPIGIQVFPLFKCKPSKNQLDKEIKYLITYVWKPGDNVSLVSDKFGASPEDIMS	207
+ N P+ + + C C ++ + K+ +TY +P D++S ++ G S DI+		
Sbjct 137	PATN-IPLSATLNVLNCSCGDES-VSKDFGLVTYPLRPEDLSIARISSGVSA-DILQ	193
Query 208	ENNYCQNFTAANNL--PVLPVTRLPVLARSPSDGRKGIRLPLVIIIGISLGCTLLVLV	264
N G NF + N + P P P S DG G VI GI +G + +L++		
Sbjct 194	RYNPGVNFNSNGNIVYVPGDPNGAFPPFKSSQDGVGAG---VIAGIVIGVIVALLI	249
Query 265	AVLLVYVYC-----LKMKTLNRSASSAETADKLLSGVSGYVS----KPTM	305
++ Y Y L K + S+S ++ +GVS ++ K		
Sbjct 250	LFIVYYAYRKNSKGDSFSSSIPLSTKADHASSTSLSQSGGLGGAGVSPGIAAISVDKSVE	309
Query 306	YETDAIMEATMNLSSEQCKIGE---SVYKANIEGKVLAVKRFKEDVTE---ELKILQKV	357
+ + + AT N + KIG+ +VY A + G+ A+K+ + ++ ELK+L +V		
Sbjct 310	FSLEELAKATDNFLNSFKIGQGGFGAVYYAELRGEKAIAKKMDMEASKQFLAELKVLRV	369
Query 358	NHGNLVKLMGVSSNDGNCFVVYEYAENGSLDEWLFSKSCSDTSNSRASLTWCQRISMAV	417
+H NLV+L+G + G+ F+VYEY ENG+L + L + R L W +R+ +A+		
Sbjct 370	HHVNLVRLICYCYVE--GSLFLVYEEVENCNLGQHLHG-----SGREPLPWTKRVQIAL	420
Query 418	DVAMGLQYMHEHAYPRIVHRDITSNNSNLFKAKIANFSMAR-----	461
D A GL+Y+HEH P VHRDI S+NIL+D F+AK+A+F + +		
Sbjct 421	DSARGLEYIHEHTVFPVYVHRDIKSANILIDQKFRAKVADFGILTLEVGGSATRGAMGTF	480
Query 462	-----TFTNPMMPKIDVFAFGVVLIELLTGRKAMTTKENGEVVMLWLDIWKIFDQ---E	512
T + + + K+DV+AFGVVL EL++ + A+ E V ++ + + +F++ E		
Sbjct 481	GYMAPETVYGEVSAKVDVYAFGVVLYELISAKGAVVKMT--EAVGEFRLGVGFEEFKE	538
Query 513	ENREERLKKWMDPKLESYYPIDYALSLASLAVNCTADKSLSRPTIAEVLSLSLL	567
+ +EE L+K +D+P+L YP D +A L CT + + RB++ IV++LS L		
Sbjct 539	TDKEEARLKIIDPRLGDSYPFDSSVYKMAELGKACTQENAQLRPSMRYIVVALSTL	593

>**emb|CBI40054.3| unnamed protein product [Vitis vinifera]**
Length=672

Score = 234 bits (598), Expect = 2e-59, Method: Compositional matrix adjust. Identities = 181/631 (28%), Positives = 297/631 (47%), Gaps = 69/631 (10%)

Query 14	IILCLVIMLFSTNIVAQSQQDNRTNFSCPSD-SPPSCETYVTVYIAQSPNFLSLTNISNIFD	72
IL V + + + + + + C + S C T+ S + SL N+S		
Sbjct 17	ILVFVSTLQGQSSLSETSSRDASQYYCNGNGSQKQCGTFALLRTNS-YYSSLNFLSFYLG	75
Query 73	TSPLSIARASNLEPMDDKLVKDQVLLPVPTCGCTGNRSFANISYEINQGDSFYFVATTSY	132
IA A+ + L + LL+P+ C C A++ +G+SF+ +A S		
Sbjct 76	IDRFLIAEANGFSADTEPLLIPNLLIPIECKCKAGFFQAEI LTIEGESFFGIAE-SL	134
Query 133	ENLTNWRAVMMDLNLVPLSPNKLPIGIGQVFPLFKCKPSKNQLDKEIKYLITYVWKPGDNVS	192
E IT +A+ + NP + P L + + + PL C CPS ++ L +E K L+Y GD V		
Sbjct 135	EGLTTCKAIRERNPSIQPWGGLADKVRLLIPLRCACPSSSELIQETKLLLSYPVSEGDTVP	194
Query 193	LVSDKFGASPEDIMSENNY-GQNFTAANNLP--VLIPVTRLPVLARSPSDGRKGIRLPV	249
+ +KF + E +S NN G + P + +P T +PV+ +P + + + V		
Sbjct 195	SLAFKFNTTSEAIISANNRSGATLRLGSAPPNLGLPATSIPIV--NPHKKKTKMWKIGV	252
Query 250	II---GISLGCTLLVVLAVLLVY-----VYCLKMKTLNRSASSAETA	289
I G+++G ++ + AVL++ + L ++T + S E +		
Sbjct 253	YIAVSGVAVGASV-AIAAAVLVIHWKRKKQNAKYMGDVELQQLGLSVRTSEKKVSFEGS	311
Query 290	DKLLSGVSGYVSKPTMYETDAIME---ATMNLSSEQCKIGESVYKANIEGKVLAVKRFKED	346
+ + + ET + +E AT + + I SV+ + GK IA+K +		
Sbjct 312	QDPIDQIIDSTPHKIVVETYTMLERLKATEDFNSSNLIEGSVFHGRNLNGKNIAKHTHPE	371
Query 347	VTE--ELKILQKV--NHGNLVKLMGVSSNDGNCFVVYEYAENGSLDEWLFSKSCSDT--	400
E + +H N++ +L+G + + + + +EYA+NGSL +WL +		
Sbjct 372	AISKIEFGLFHDAIHHPNIMRLLGTCLNEGPDSLYLIFEYAKNSLKDWLHGGLAMKSQF	431
Query 401	-SNSRASLTWCQRISMAVDVAMGLQYMHEHAYPRIVHRDITSSNILLDSNFKAKIANFSM	459
+ + LTW QR+ + DVAM LQYMH + P VHR+I S NI LD F AKI NF M		
Sbjct 432	IASCYCFLTWNQRLRICLDVAMALQYMHIMHPCYVHRNIKSRNIFLDEFNAKIGNFGM	491
Query 460	ARTFTNP-----MMPKIDVFAFGVVLIELLTGRKAMTTK	493
AR F + + P +D+FA+GVVL+E+L+G+ +T		
Sbjct 492	ARCFEDDAEDSQPYSTASWSKGYLAPEYLHQGIIISPTLDIFAYGVVLEVLSGKTPITRA	551
Query 494	EN--GEVVMLWKDIWIKEFQEENREERLKKWMDPKLESYYPIDYALSLASLAVNCTADKS	551
++ G V L + I I E E L + WMD L Y D A++IA+LA CT +		
Sbjct 552	DDKGGRVWLPEKIKSILGSENT--EELRDWMD SALGENYSFDAIITLANLARVCTDENP	609
Query 552	LSRPTIAEVLSLSLLTQSPATLERSLTSS	582
SRP+ EIV LS L + P + S+ S		
Sbjct 610	CSRPSAGEIVEKLSLRLVEQLPEGEQFSICES	640

>**ref|XP_002263070.1| PREDICTED: hypothetical protein [Vitis vinifera]**
Length=675

Gene ID: 100264694 LOC100264694 | hypothetical protein LOC100264694 [Vitis vinifera] (10 or fewer PubMed links)

Score = 233 bits (595), Expect = 4e-59, Method: Compositional matrix adjust. Identities = 185/652 (28%), Positives = 298/652 (45%), Gaps = 89/652 (13%)

Query 14 ILCVIMLFSTNIVAQSQQDNRTNFSCPSD-SPPSCETYVTVYIAQSPNFLSLTNISNIFD 72

Sbjct	17	IL V L + + ++ + + C + S C T+ S + SL N+S ILVFVSTLGQSLSLSETSSRDAAGYYCNGNGSQKQCGTFALLRTNS-YYSSLFNLSFYLG	75
Query	73	TSPSLSIARASNLLEPMDDKLVKDQVLLPVTCGCTGNRSFANISYEINQGDSFYFVATTSY IA A+ + L + LL+P+ C C A ++ +G+SF+ +A S	132
Sbjct	76	IDRFLIAEANGFSADTELLPYNPLLIPIECKCKAGFFQAELTKTTIEGESFFGIAE-SL	134
Query	133	ENLTNWRAVMDLNPNVLSPNPKLPIGIQVVFPFLFKCPSKNQLDKEIKYLITYVWKPGDNVS E IT +A+ + NP + P L + + + PL C CPS ++L +E K L++Y GD V	192
Sbjct	135	EGLTTCKAIRERNPSIOPWGLADKVRLLIPLRCACPSSSELIQETKLLLSYPVSEGDTVP	194
Query	193	LVSDFKFGASPEDIMSENNY-CQNFTAANNLPV---LIVVTRLPVLARSPSDGKRGGIRLP ++ KF + E I+S NN G + PV LIP+ P L SP+ R+ + LP	248
Sbjct	195	SLAFKFNTTSEAI1SANNRSGATLRLGS LAPVSSLITPLRDKEPTLG-SPAKPREPNLGLP	253
Query	249	V-----IIGISLGCTLLVVLVLAVLVLY----- + G+++G ++ + AVL+++	270
Sbjct	254	ATSIPIVINPHKKTKMWKIGVYIAVSGAVGASV-AIAAAVLVIHWKRKKQNAKMGDVE	312
Query	271	--VYCLKMKTLNRSASSAETADKLLSGVSGYVSKPTMYETDAIME---ATMNILEQCKIG L ++T + S E + + + + ET ++E AT + + I	325
Sbjct	313	LQQLGLSVRTTSEKKVSFEGSQDPIDQIIDSTPHKIVVETYTMLERKATEDFNSSNLIE	372
Query	326	ESVYKANIEGKVLAVKRFKEDVTE--ELKILQKV--NHGNLVKLMGVSSNDGNCVVYE SV+ + GK LA+K + E + +H N++L+G + + ++++E	381
Sbjct	373	GSVFHGRNLNGKNLAIKHHTPEAISKIEGLFHDAIHHPNIMRLLGTCLNEGPDSYLIFE	432
Query	382	YAENGSLDEWLFSKCSDT---SNSRASLTWCQRISMAVDVAMGLQYMHEAYPRIVHRD YA+NGSL +WL + ++ LTW QR+ + +DVAM LQYMH +P VHR+	438
Sbjct	433	YAKNGSLKDWLHGGLAMKSQFIASCYCFLTWNQRLRICLDMVALQYMHMHPCYVHRN	492
Query	439	ITSSNILLDSNFKAKIANFSMARTFTNP-----MMPKID I S NI LD F AKI NF MAR F + + P + D	472
Sbjct	493	IKSRNIFLDEENFAKIGNFGMARCFCEDDAEDSQPYSTASWSKGYLAPEYLNHQGIISPALD	552
Query	473	VFAFGVVLIELLTGRKAMTTKEN--GEVVMLWWDIWKIFDQEENREERLKKWMDPKLESY +FA+CVVL+E+L+G+ +T ++ G V L + I I E E L+ WMD L	530
Sbjct	553	IFAYGVVLLEVLSGKTPITRADDKGGGRVWLPEKIKSILGSENT--EELRDWMDALGEN	610
Query	531	YPIDYALSLASLAVNCTADKSLSRPTIAEIVLSSLTQPSPATLERSLTSS 582 Y D A++LA+LA CT + SRP+ EIV LS L + P + S+ S	
Sbjct	611	YSFDAAITLANLARVCTDENPCSRPSAGEIVEKLSRLVEQLPEGEQFSICES	662

Select All Get selected sequences Distance tree of results Multiple alignment

APPENDIX C

Claim	Type	Depends from	%ID	AA SEQ ID	NA SEQ ID
59.	AA	-	80 AA	8 15 31 32 40 48	-
60.	AA	-	80 AA	24 25	-
61.	AA	59	100 AA	8 15 31 32 40 48	-
62.	AA	60	100 AA	24 25	-
63.	AA-combo	59 + seq	80/80 AA	8 15 31 32 40 48/ 24 25 52 54	-
64.	AA-combo	61(59)	100/100 AA	8 15 31 32 40 48/ 24 25 52 54	-
65.	NA	59	80 AA	ENC 80%[8 15 31 32 40 48]	-
66.	NA	60	80 AA	ENC80%[24 25]	-
67.	NA	65 (59)	100 NA	[encode 80% 8 15 31 32 40 48]	6 7 11 12 30 39 47
68.	NA	66 (60)	100 NA	[encode 80% 24 25]	21 22 23
69.	Tg cell NA	59	80 AA	[encode 80% 8 15 31 32 40 48]	-
70.	Tg cell NA	69(59)	100 AA	[encode 100% 8 15 31 32 40 48]	-
71.	Tg cell NA	69(59)	100 NA	[encode 80% 8 15 31 32 40 48]	6 7 11 12 30 39 47
72.	Tg cell NA	60	80 AA	ENC80%[24 25]	-
73.	Tg cell NA	72(60)	100 AA	ENC100%[24 25]	-
74.	Tg cell NA	72(60)	100 NA	ENC 80%[24 25]	21 22 23
75.	Tg cell NA	63(59)	80/80 AA	[enc 8 15 31 32 40 48/ 24 25 52 54]	-
76.	Tg cell NA	63(59)	100/100 AA	[enc 8 15 31 32 40 48/ 24 25 52 54]	-
77.	plant cell	Xxx			
78.	plant cell	Xxx			
79.	plant cell	Xxx			
80.	plant cell	Xxx			
81.	plant cell	Xxx			
82.	plant cell	Xxx			
83.	plant cell	Xxx			
84.	plant cell	Xxx			
85.	method	59	80 AA	8 15 31 32 40 48	-
86.	method	85(59)	100 AA	8 15 31 32 40 48	-
87.	method	85(50)	100 NA	[encode 80% 8 15 31 32 40 48]	6 7 11 12 30 39 47
88.	method	60	80 AA	24 25	-
89.	method	88 (60)	100 AA	24 25	-
90.	method	88(60)	100 NA	[encodes 80% 24 25]	21 22 23
91.	method	85(59)	80/80 AA	[8 15 31 32 40 48/ 24 25 52 54]	-
92.	method	86 (85)(59)	100/100 AA	[8 15 31 32 40 48/ 24 25 52 54]	-
93.	method	91(85)(59)	100 NA	[encodes 80% 8 15 31 32 40 48/ 24 25 52 54]	6 7 11 12 30 39 47/ 21 22 23 51 53
94.	Method x	85(59)	80 AA	8 15 31 32 40 48	-
95.	Method x	88(60)	80 AA	24 25	-
96.	Method x	91(85)(59)	80/80 AA	[8 15 31 32 40 48/ 24 25 52 54]	-
97.	Method x	93(85)(59)	100 NA	[encodes 80% 8 15 31 32 40 48/ 24 25 52 54]	6 7 11 12 30 39 47/ 21 22 23 51 53
98.	Tg plant	59	80	8 15 31 32 40 48	-
99.	Tg plant	98(59)	100	8 15 31 32 40 48	-
100.	Tg plant	60	80	24 25	-
101.	Tg plant	100(60)	100	24 25	-
102.	Tg plant	63	80/80	8 15 31 32 40 48/ 24 25 52 54	-
103.	Tg plant	64	100/100	8 15 31 32 40 48/ 24 25 52 54	-

Claim	Type	Depends from	%ID	AA SEQ ID	NA SEQ ID
104.	Cereal	98(59)	80 AA	8 15 31 32 40 48	-
105.	Cereal	XXX			
106.	Cereal	100(60)	80 AA	24 25	-
107.	Cereal	XXX			
108.	Cereal	XXX			
109.	Cereal	XXX			
110.	Legume	98(59)	80 AA	8 15 31 32 40 48	-
111.	Legume	XXX			
112.	Legume	100(60)	80 AA	24 25	-
113.	Legume	XXX			
114.	Legume	XXX			
115.	Legume	XXX			
116.	Non-nod	98(59)	80 AA	8 15 31 32 40 48	-
117.	XXX				
118.	Non-nod	100(60)	80 AA	24 25	-
119.	XXX				
120.	XXX				
121.	XXX				
122.	AA	-	90 AA	52 54	-
123.	NA	122	90 AA	encodes 90%[52 54]	-
124.	Tg cell NA	122	90 AA	encodes 90%[52 54]	-
125.	Tg cell NA	124(122)	100 NA	Encodes 90% [52 54]	51 53
126.	Tg plant	122	90 AA	Encodes 90%[52 54]	-
127.	Tg plant	98(59)	80 AA	8	-
128.	Tg plant	98(59)	80 AA	15	-
129.	Tg plant	98(59)	80 AA	31	-
130.	Tg plant	98(59)	80 AA	32	-
131.	Tg plant	98(59)	80 AA	40	-
132.	Tg plant	98(59)	80 AA	48	-
133.	Tg plant	100(60)	80 AA	24	-
134.	Tg plant	59	100 AA	8	-
135.	Tg plant	59	100 AA	15	-
136.	Tg plant	59	100 AA	31	-
137.	Tg plant	59	100 AA	32	-
138.	Tg plant	59	100 AA	40	-
139.	Tg plant	59	100 AA	48	-
140.	Tg plant	60	100 AA	24	-
141.	Tg plant	122	100 AA	52	-

XXX=CANCELLED CLAIM

Claim 93 depends from claim 91

Claim 125 depends from claim 124